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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: February 26, 2002, 17:50:45; Search time 8647.11 Seconds (without alignments)	Title: US-09-646-224A-1 Perfect score: 5897 Sequence: 1 ggagccatacggtgccctgagaaaaaaaaaaaaa	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1472140 seqs, 8248589755 residues	Total number of hits satisfying chosen parameters: 2944280	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1 9 b.ba:* 2 9b.htg:* 3 9b_lns:* 4 9b_on:* 5 9b_on:* 6 9b_pat:* 7 9b_pp:* 10 9b_pp:* 11 9b_sp:* 12 9b_sp:* 13 9b_un:* 14 9b_sp:* 15 em_ba:* 15 em_ba:* 16 em_fun:* 17 em_hun:* 18 em_lin:* 18 em_lin:* 19 em_ph:* 20 em_or:* 21 em_ph:* 22 em_ph:* 23 em_ph:* 24 em_ph:* 25 em_sp:* 26 em_con:* 27 em_sp:* 28 em_lin:* 29 em_htgo_lnv:* 31 em_htgo_lnv:* 32 em_htgo_lnv:* 33 em_htgo_lnv:* 34 em_htgo_lnv:* 35 em_htgo_lnv:* 36 em_htgo_lnv:* 37 em_htgo_lnv:* 38 em_htgo_lnv:* 38 em_htgo_lnv:* 39 em_htgo_lnv:* 31 em_htgo_lnv:* 31 em_htgo_lnv:* 32 em_htgo_lnv:* 34 em_htgo_lnv:* 35 em_htgo_lnv:* 36 em_htgo_lnv:* 37 em_htgo_lnv:* 38 em_htgo_lnv:* 38 em_htgo_lnv:* 39 em_htgo_lnv:* 31 em_htgo_lnv:* 34 em_htgo_lnv:* 35 em_htgo_lnv:* 36 em_htgo_lnv:*

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Dibh Haji, S.D., Tyrrell, L., Black, J.A. and Waxman, S.G.
Direct Submission
Submitted (10-APR-1998) Neurology, Yale University Medical School, 333 Cedar St, New Haven, CT 06510, USA
On Jul 16, 2001 this sequence version replaced gi:3372614.
Location/Qualifiers
                                                                                                                                                ROD 16-JUL-2001 channel alpha subunit NaN mRNA,
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Sciurognathi; Muridae; Murinae;
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/organism="Rattus norvegicus"
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Mammalia; Eutheria; Rodentia;
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Location/Qualifiers

FEATURES

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Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.
Nucleic acid encoding sodium channel of nerve tissue
Patent: JP 1999235186-A 4 31-AUG-1999;
F HOFFMANN LA ROCHE AG
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                                                                                                                                                                                                                                                                                                    Artificial Sequence
JP 1999235186-A/4
1-AUG-1999
20-NOV-1998 JP 1998331769
20-NOV-1997 US 60/06622
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                                                                                                                                       DNA
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                                                 5878
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99.7%;
                                                                                                                                                                            GI:13022508
                                                                                                                                     E36125 5334 bg
Nucleic acid encodir
E36125
E36125.1 GI:1302256
UP 1999235186-A/4.
                                                              AACGAATAAATAGGTAAAAG
                                                  aacgaataaataggtaaaag
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Best Local Similarity
Matches 5304; Conserv
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 5799
                       5829
                                                                         5889
                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
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A GAMB
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STLRTFRVLRALKAISVISGLKVIVGALLRSVKKLVDVMVLTLFCLSIFALVGQQLFM
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5823. ,5828
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                        sodium channel"
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88.4%;
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Sciurognathi; Muridae; Murinae; Mus
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Dib-Haji,S.D., Tyrrell,L. and Waxman,S.G.
Direct Submission
Submitted (05-JAN-1999) Neuroscience Research Center, 127A, Yale
University/VAMC, 950 Campbell Ave, West Haven, CT 06516, USA
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Mus musculus voltage-gated sodium channel NaN (Scn11a) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgaccgcctccattgcatggatgttctctttgctttcactaccagggtcctcggggactc
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                                                                                catgtacatcgctgtgatcctcgagaacttcaacacagccacggaggaggaggaccc
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 5858)
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Dib-Hajj,S.D., Tyrrell,L., 1
Waxman,S.G.
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KEYWORDS
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12;

Gaps 66

78;

159

163 219 223 279

103

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Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman,S.G. Direct Submission
Submitted (21-SEP-1999) Naurolon Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1, Chases 1 to 6237]
Dib-Haji,S.D., Tyrrell,L., Cummins,T.R., Black,J.A., Wood,P.M. and Waxman,S.G. 5429 5489 5549 5610 5669 5842 5860 AF188679 6237 bp mRNA PRI 14-DEC-1999 Homo sapiens voltage-gated sodium channel type XI alpha subunit (SCN11A) mRNA, complete cds. root 5372 5369 5432 5490 5550 5609 5723 5744 5782 5804 -----TCTGTTCAGTTTAA 5684 GCCGTTCAACTTGTTTTTTGGGTGAAAGAGGTGATAGGTTGGTGTCCATTTTTAAATGA Two tetrodotoxin-resistant sodium channels in human dorsal gccgttcgatctgtgtttttggctgaacgaggtgacaggttggcgtccatttttaaatga aggotgaaggacaggtcaagttcatcgcaccaggtgttttgcaatggagacttgtccagc acggaaggcctggaggacagtccaacttacataaagatgagaaacaagaaggaaagatcc caggaaaacttcagattgtgttctcagtacattccccaatgtgtctgttcggtgttttga gtatgtgacctgccacatgtagctcttttttgcatgtac----gtcaaaaccctgcag d (21-SEP-1999) Neurology, Yale University/VAMC, 950 Campbell Ave., West Haven, CT 06516, USA Location/Qualifiers
1. .6237
/organism="Homo sapiens"
/db_xref="taxon:9606" ganglion neurons FEBS Lett. 462 (1-2), 117-120 (1999) 20047838 CATG ÀF188679 AF188679.1 GI:6572949 Homo sapiens Bldg.34, . human. VERSION KEYWORDS SOURCE ORGANISM source DEFINITION JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL 5433 5251 5313 5311° 5373 5370 5430 5491 5490 5551 5550 5610 9999 5670 5685 5724 5745 5783 5805 5843 5861 ACCESSION REFERENCE AUTHORS RESULT AF188679 FEATURES TITLE LOCUS ್ನಾರಿಗಳ ಕಿ.ಬರ್. ರಿ.ಬರ್. ರಿ.ಬರಿ. ರ್ಬರಿಸಿರ ರಿ.ಬರಿಸಿರು ಹಿಚ್ಚಾರಿಸಿ ರಿಸ್ಟರ್ ಜಿನ್ ಸರ್ಕಿಸಿ

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Conservative
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                          5'UTR
                                            gene
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\$ a	1875 ggttttcacgggaatttcatagcggaaatgtgtctcaagatcatcgcgctcgaccctta 1934 	
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224a-1.rge

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Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,
Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I.
Identification of a novel human voltage-gated sodium channel alpha
                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ogy, Graduate School of Medicine,
Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channel alpha subunit
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Jeong,S.Y., Suzuki,T., Hashida,H., Masuda,N., Goto,J. and
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Submitted (27-NOV-1998) Neurology,
Tokyo University, 7-3-1 Hongo, Bunk
                                                                                                                                                                                                                                                                                                                                                   Biophys. Res. Commun. 267
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   AF109737.1
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                                                                                              Homo
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AUTHORS
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MEDLINE
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VERSION
KEYWORDS
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BASE COUNT 1842 a 1446 c 1410 g 1830 t
ORIGIN
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Length 6528;

6

В

Score 3234.2; Pred. No. 0;

54.8%; 76.2%;

Query Match Best Local Similarity

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Wed Feb

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DB 9 :: Length 5728;

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Similarity
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Matches 3316;
                                          Query Match
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KLICKNYTNIKIIGNGVALGENTYVVLVIVIFFSVVGWQLFGRSFRVRTAK
KLIVALNIKIIALINGSSNEERNGNLEGERARTKVQLALDRFRRAFCFYK
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LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 5728)
Jeong, S. Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,
Identification of a novel human voltage-gated sodium channel alpha
subunit gene, SCN12A
Blochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
20090626
C (bases 1 to 5728)
Jeong, S. -Y., Suzuki, T., Hashida, H., Ogata, K., Masuda, M., Goto, J.
and Kanazawa, I.
                                                                                                                                         AFI50882 5728 bp mRNA PRI 15-JAN-2000 Homo sapiens voltage-gated sodium channel alpha subunit, alternate splice variant SCNI2A-s (SCNI2A) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,
Tokyo University, 7-3-1 Hongo, Bukyo-ku, Tokyo 113-8655, Japan
Location/Qualifiers
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alternate splice variant SCNI2A-s"
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    . 5728
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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                                      954: Findels
Score 2585.6;
Pred. No. 0;
0; Mismatches
43.8%;
illarity 76.3%;
Conservative
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n.v.	212		235	22	71	228	DD 2471 T	253	Óy 2401 g pb 2591 G	Qy 2461 g	Oy 2521 o	y 2581 t	- 56		Oy 2688 -	Oy 2731 c		0E . 6	307	3 8	(4) W	Oy 3031 a f: Db 3248 P	Oy 3091 t	er care
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151 GGTAACAGTGCCTGTTCCATACAATATGAATGTAAGCACAAAAATTAATCCTGACTAT 1210	45 aattatacaaagtttgacaactttggctggtcctttctcgccatgttccgggttatgact 110		05 caagactectgggagaggetttacegacagatectgeggaeetetgggatetactttgte 116	71 CAAGATTCCTGGGAGAAGCTTTATCAACAGACCCTGCGTACTACTGGGCTCTACTCAGTC 133	165 ttettettegtggtggtcatetteetgggeteettetaectgettaacetaaeeetgget 1224 31	25 gttgtcaccatggcttatgaagaacagaacagaaatgtagctgctgagacagaggccagg 128	IIII IIIIIIIIIII SAGATAGAGGCCAA	285 gagaaatgtttcaggaagcccagcagctgttaagggagagaaggagctctggttgcc 1344 	45 atgggaattgacagaagttcccttaattcccttcaagcttcatccttttccccgaagaag 140 	05 aggaagtttttcggtagtaagacaagaaagtcttctttatgagagggtccaagacggcc 146	caagcetcagcgtctgattcagaggacgatgcctctaaaaatccacagctccttgagcag 152	25 accaaacgactgtcccagaacttgccagtgatctctttgatgagcacgtggacccctc 158	CACTGTCCCAGAATCTATCACTGGACCACTTTGATGAGCATGGAGATCCTCTC 175	0 10	645 aaattccaggagccttgtttogcatgtgggaaaaatttggcctctaagtacctggtgtgg 1704 	05 gactgtagcctcagtggctgtgcataaagaagtcctgcggaccatcatgacgatcc 176	TGTTGCCCCCAGTGGCTGTGTGTTTTTTTTTTTTTTTTT	765 tttactgagctggccatcaccatctgcatcatcatcaataccgttttcttagccgtggag 1824 	825 caccacaacatgatgacaacttaaagaccatactgaaaataggaaactgggttttcacg 1884 	85 ggaattttcatagcggaaatgtgtctcaagatcatcgcgctcgacccttaccactactc 19 	ctcctgagtctcgctgatg1 	2005 tacaacacactgtctgataacaataggtctttcttggcttccctcagagtgctgagggtc 2064 	065 ttcaagttagccaaatcctggcccacgttaaacactctcattaagatcatcggccactcc 2124 	
Db 1	-	-	н		Oy 111	١ ٦	Db 1:	Oy 121	7 7		п -			Db 17	0y 10	-	Db 11	Oy 17 Db 19	0y 11 da	Oy 181	Oy 1	Oy 2	Oy 20	

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NWFETFIVFMILLSSGALAFEDIYIEQRRVIRFILEYADKVFTYIFIMEMLLKWVAYG
FKVYFTNAWCWLDFLIVDVSIISLVANWLGYSELGPIKSLRTLRALRPLRALSRFEGM
                                                                                                                                      HUMSKMIA 7823 bp mRNA PRI 13-JAN-1995
Homo sapiens skeletal muscle voltage-dependent sodium channel alpha
subunit (SkM1) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLGEADGAGEAGEAGETAPEDEKKEPPEEDLKKDNHILNHMGLADGPPSSLELDHLNF
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George, A.L. Jr., Komisarof, J., Kallen, R.G. and Barch.
Primary structure of the adult human skeletal muscle
voltage-dependent sodium channel
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transmembrane protein; voltage-dependent sodium
subunit.
                                                                                                                                                                                                                                    Homo sapiens adult skeletal muscle cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="skeletal muscle"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Euteleostomi;

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and Barchi, R.L.

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IYSIFGMSNFAYVKKESGIDDMFNFETFGNSIICLFEITTSAGWDGLLNPILNSGPPD
CDPNLENPGTSVKGDCGNPSIGICFFCSYIIISFLIVVNMYIAIILENFNVATEESSE
PLGEDDFEMPYETWEKFDPDATQFIKYSRLSDFVOTLQCPFTARPNKIKLITLDLPM
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PEVCANIKIQANSTRHLLGRSWQASYMYRHSHDGSGDDAPEKEGLLANTMSKNYGHEN
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Sangameswaran, L. Delgado, S.G., Fish, L.M., Koch, B.D., Jakeman, L.B., Stewart, G.R., Sze, P., Hunter, J.C., Eglen, R.M. and Herman, R.C. Structure and function of a novel voltage-gated, tetrodotoxin-resistant sodium channel specific to sensory neurons J. Biol. Chem. 271 (11), 5953-5956 (1996)
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RIQVLGHRASRAIASYISSHCRFRWFKVETQLGMKPPLTSSBAKNHTATDAVSAAVGN
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TVDCPDPEEILRKIPELADDLDEPDDCFTEGCTRRCPCCNVNTSKSPWATGWQVRKTC
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RFSATWALWLFSPFNLIRRTAIKVSVHSWFSIFITITILVNCVCMTRTDLPEKVEYVF
TVIYTFEALIKILARGFCLNEFTYLRDPWNWLDFSVITLAYVGAAIDLRGISGLRTFR
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YTSFDSFAWAFLSLFRLMTQDSWERLYQQTLRASGKMYMVFFVLVIFLGSFYLVNLIL
AVVTWAYEEQSQATIAEIEAKEKKFQEALEVLQKEOEVLAALGIDTTSLQSHSGSPLA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteléostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muripae;
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Sangameswaran,L.B., Delgado,S.G., Fish,L.M., Koch,B.D.,
Jakeman,L.B., Stewart,G.R., Sze,P., Hunter,J.C., Eglen,R.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herman, R.C.
Additions and corrections to structure and function of a novel
voltage-gated, tetrodotoxin-resistant sodium channel specific
                                                           20-JUN-1996
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                                                        RNU53833 6344 bp DNA ROD 20-JUN
Rattus norvegicus sodium channel PN3 gene, complete cds.
U53833
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2 (bases 1 to 6344)

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Sciurognathi; Muridae; Murinae; Mus.
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Zimmer.T. and Benndorf, T.
The mouse heart sodium channels: cloning and characterization of two distinct isoforms and alternatively spliced variants
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Mus musculus mRNA for voltage-gated
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Friedrich Schiller University J
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SCN4A gene; voltage-gated
house mouse.
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1681	1788	1848	1908	1968 1921	2028	2088	2148	2208	2265	2325	2385	2445	2505	2565	2625 2569	2685	2745	2805
qq	Qy Dp	Qy	Qy Dp	Qy	Qy Dp	Qy Db	Qy Db	Qy Dp	Oy Dp	Oy Dp	Qy	QY	QY Dp	Qy Dp	Qy Db	Qy Db	Qy	Qy

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Qy 4971 gccgaataagtttcagtttctagtgatgacttgcccatggtgatggcgaccgcctca 5030 11 11 11 11 11 11 11	14 TION ION N DS	SOURCE unidentified. COGANISM unidentified. Notable Service (bases 1 to 6527) CATTLE ION CHANNEL JOURNAL PAtent: WO 9701577-A 7 16-JAN-1997; FEATURES SOURCE / Adams = 1 . 6527 / Adams = 1 . 6527	CDS 204 6077 // note=-"unnamed protein product" // codon_start=1 // protein_id="CAA03509.1" // protein_id="CAA03509.1" // protein_id="CAA03509.1" // db_xref="dg:3714381" // translation="MELPFASVGTINFRFTPESLAEIEKQIAAHRAAKKARTKHRGQ EDKGEKRPRQLDIKLOKOYUPFKYGELPAEIVGEPLEDLDPPYSTHRTFMYLMKSRTIS RFSATWALWLESPFNLIRRTAIKVSVHSWFSIFTITIUVNCVCMTRTDLDEKVEVVF TVIYTFEALKILIENGRCLINEFYLRDPWNWLDFSVITALAVVGAADLEKGISGLRFR VLRALKTVSV1FGLKKVITARGFCLINEFYLRDPDMNWLDFSVITALAVVGAALVGLQLFKGNLKNKC IRNGTDPHKADNLSSEMAEYIFIKPGTTDPLLCGNGSDAGHCPGGYVCLKTPDNPDFN YTSFDFSFRAMFLELEFRLAVTQDSHERLYQCTLRASGKWMYPFVULTFLGSFVLVNLLIL AVVTMANYPFOGGATIAFTRE REKEKFOFAL FULLIL	SKNANERPRYKERVESCTDONS PROCHECTORY CONTROLL 15 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	STUDCPDPEEILRKIPELADDLDEPDDCFTEGCTRRCPCCNNNTSKSPMATGMOVRKT CYRIVERBEWEEST IFMILLSSGALAFEDNYLEBRENKSVLETYDRVFTFT FVFEML LKWAYGFKKFTNAMGWLDELINSLIAKILEYSDVASIKALRTBALRALRA LSRFEGMRVVYDALAGATESIMNYLLFSIMGYNLFAGKFSKCVDTRNDP SNVNSYNWNNKSECHONSTGHFFWYNKYKPTALLQVATFKGMMDIWAA VDSGEINSOPNWENNLYWYLFVYPTIFGGFFTIMLFVGYIIDNFNQOKKKLGGODIF MTEEOKKYYNAMKKLGSKPORPTPRDLKYQGFFTIMLFVGYIIDNFNQOKKKLGGODIF MTEEOKKYYNAMKKLGSKPORPTPRDLKYQGFFTINLFVGYIIDNFNQOKKKLGGODIF MTEEOKKYYNAMKKLGSKPORPTPRDLKYQGFFDIILFVGYIIDNFNGOKTLNIT MAVETDEQGEKTKVLGRINGFFPRDLKYQGFFDIILFNGWYFDFIVVILS IGSLLFSAILKSLENYFSPFILFRVIRLARAGGIRTLLFALMMSLPALF
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1 to 5523)
Stewart,D., Fraser,S.P., Black,J.A., Dib-Hajj,S.,
.., Archer,S.N. and Djamgoz,M.B.
.. of skeletal muscle-type voltage-gated Na+ channel in rat
prostate cancer cell lines
427 (1), 5-10 (1998)
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(21-APR-1998) S.N. Archer, International Marine Centre, as Mardini, 09072 Torregrande, Oristano, ITALY Location/Qualifiers
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                              sctgccggagccgttgcgtgtggccaagccgaataagtttcagtttct 4991
jtttgaccccgaggcgtcgcagttcatccagtattcggccctctctga 4931
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                                                                                                                                                                                                                                                                                                           GEKGPPRESCSADSAISDAMEELEBAHOKCPPWWYKCAHKVLIWNCCAPWVKFKHIIY LIYWDPWDAGAITCIYULNTEMAMBHYPWTBERDVULSGWINFGTGIFTAEMUKLI LAUMDPFWDAGAITCIYULNTLEMABHYPWTBERDVULSGWINFGTGIFTAEMUKLI LAUMDPYBYFQQGWINFDSFIYTLIXUBLGLAWVQGLSYLKSFRLLKSFKLLKPREPTLUM LIKIIGNSVGALGNLTLVLAIIVFIFAVVGWQLFGKSYKECVCKIASDCNLPRWHMND
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PGTNVRGDCGNPSIGICFFCSYIIISFLIVVNMYIAIILENFNVATEESSEPLSEDDF
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QGEEEKASTEDAGPTVEPKPTSSSDTALTPSPPPLPPSSSPPQGQTVRPGVKESLV"
                                                                                                                                                                                                                       YINDEGNFYFLEGSNDALLCGNSSDAGHCPEGYECIKAGRNPNYGYTSYDTESWAFLA
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Length 5523;

Score 1403.4; DB 10; Length 5523 Pred. No. 0;); Mismatches 2116; Indels 132;

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Query Match 23.8%; Best Local Similarity 57.1%; Matches 2995; Conservative (

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m for}$ English protein 52-58; 73pp; channel sodium Page 4 Claim

2a (SNS-2a). a method for for assaying modulators The present sequence encodes rat sensory neurone specific 2a SNS-2a is a sodium channel protein. SNS-2a can be used in a mathe identification of a modulator of a sodium channel, and for compounds which modulate sodium flux. The sodium channel can be used in a medicament for the treatment of pain or hypersensitivity.

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	4141 g 4141 g	4201 ttcgtgg 4201 ttcgtgg	4261 ttcaccaatggctggaacttatttgattgtgtggtcgtggttctttct	4321 ctggtttcccgcttggaggacagtgacatttctttcc 	4381 cgcttggctcggattggtcgaatcctcaggctggtccgggctgccgggggggflllllllllllllll	4441 ctcctcttgctttgatgatgtctctccctctctctcaacatcggtctgc	4501 ctggtgatgttcatttacgccatctttgggatgagctggttttccaaagtg	4561 tccgggatcgacgacatcttcaactttcgagacctttacgggcagcatgctgtgcctcttc 462	4621 cagataaccacttcggctggctgggtaccctcctcaaccccatgctggaggcaaaagaa 468	4681 cactgcaactcctcctccaagacagtgtcagcagcagcagatagccgtctacttc 474	4741 gt 4741 gt	4801 9 4801 9	4861 atcttctatgaggtctgggagaagtttgaccccgaggcgtcgcagttcatccagtattcg 4920 	4921 gccctctctgactttgcggacgccctgccggagccgttgcgtgtggccaagccgaataa 	4981 tttcagtttctagtgatgaacttgcccatggtgatgggcgacgcctccattgcatggat 504 411111111111111111111111111111111111	5041 gttctctttgctttcactaccagggtcctcggggactccagcggctttggataccatgaaa 510	5101 accatgatggaggagaagtttatggaggccaaccttttaagaagctctggacaccacgaaa old 5101 accatgatggaggagaagtttatggaggccaacccttttaagaagctctacgagcccata 516 65101 accatgatggagagaagtttatggaggccaaccctttttaagaagctctacgagcccata 516 65101 accatgatgatggagagagagtttatggaggccaaccctttttaagaagtttaggagagaga	5161 gtcaccaccaccacagaggaaggaggaggagcaaggcgccgtcatcagaggcctac 522
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5460 5460 5280 aggagcaaggcgccgccgtcatccagagggcctac 5220 odotoxin resistant; pain; y; analgesic; vaccine; gene therapy; fiers 360

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ರಿ ನೀರಿ ರೀರು ರೀರು, ರೀರೀರಿ ರೇವಿ ಎರಡುವ ಮಾರುವಿದ್ದರು.
                                                                                                                                                                                                                                                                                          The present sequence is that of cDNA encoding a novel rat tetrodotoxin resistant sodium channel, termed NaN (see AAB20122). The cDNA was isolated from a dorsal root gangliat issue cDNA ilbrary by PCR amplification using generic primers (from conserved resions of a-subunit sodium channel, proteins) and NaN-specific resions of a-subunit sodium channel, proteins) and NaN-specific copen reading frame shows 738 similarity to the human NaN sequence open reading frame shows 738 similarity to the human NaN sequence (see AAF30101). NaN belongs to the a-subunit voltage-gated sodium channels underlie the generation and propagation of impulses in channels underlie the generation and propagation of impulses in expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other therapeutic uses in relation to acute and/or thronic pain pathologies. A claimed method of treating pain, paraesthesia nod/or hyperexcitability phenomena in a human or animal subject involves administering an agent that allers sodium current flow through NaN channels, or which modulates transcription or translation of NaN mannels or parts of ganglia or triggminal
                                                                                                                                                                                                                    sodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nel expression or
the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or
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                                                                                                                                                                                                                               channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -
                                                                                                                                                                                                                  resistant
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                                                                                                                                                                                                                    molecules encoding human tetrodotoxin
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ó 248 188 240 368 300 89 9 0; Gaps tgacattccccctgagcttgttacgaaacctctggaggacctggacccctactacaaaga acggtgccctgatcctctgtaccaggaagacaggtgaagatggaggaggggactaccc acggtgccctgatcctctgtaccaggaagacagggtgaagatggaggaggggaggtactacc aaagaagcggattgctatccaaaaggagagaagaagtccaaagacaaggcggcagctga agagaagcggattgctatccaaaaggagagagaagaagtccaaagacaaggcggcagctga Coataagacattcatggtgttgaacaagaaaagaacaatttatcgcttcagcgccaagcg gccccagcctcggcctcagcttgacctaaaggcctccaggaagttacctaagctttatgg gececagecteggeeteagettgaectaaaggeetecaggaagttaectaagetttatgg Length 5875 Indels 22; 14; DB Score 5853.8; 0; Mismatches No. 0; Pred. 99.3%; Similarity 99.8 11; Conservative Best Local Simmatches 5861; Query Match φ 69 61 129 121 189 181 249 241 309

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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ilarity 99.8%;
Conservative
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P-PSDB; AAY16572.
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Matches 5829; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids encoding sodium channels, used to develop treating acute or chronic pain or hyperexcitability
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                                            ctctgacttgtcagtcagcaccccgactttcagacgctccaatctctgtcccaggtgtct
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from the sequence given in Fig 1 of the
specification. The nucleotides are
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Scn11a gene;
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numbering given in the specification
this DNA sequence"
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paraesthesia; hyperexcitability; therapy;
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channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The NaN gene has been named Scnlla. that express NaN, methods for it channel activity or NaN channel and a method for using such age and amethod for using such age or areasthesia and hyperexcitability paraesthesia and hyperexcitability contained for selectively modifying the nanget for selectively modifying the nanged sort while not affecting other nerved to while not affect and the nerved to while not affect the new manual to the nerved to while not affect the new manual to the new manual to

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al root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
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1999-315739/27
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system nervous the oţ sodium channel Isolated DNA encoding

90pp; French. 5A-E; Fig Example

The present sequence encodes a type 5 sodium channel protein designated PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, tranmatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache

Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 other

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Length 5334;
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              Indels
DB 20;
              14;
Score 5295.6;
Pred. No. 0;
0; Mismatches
89.88;
99.78;
              Conservative
       Similarity
              Matches 5304;
Query Match
       Local
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                                                     ggacaggtcaagttcatcgcaccaggtgttttgcaatggagacttgtccagcttggatgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sodium channel; NaN; Scnlla; mouse; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                communers, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena
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5789..5794
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for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct indisorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                Length 5822;
                                                                                                                                                                                                                                   in the recombinant production of NaN polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                     BP; 1499 A; 1425 C; 1362 G; 1535 T; 1 other;
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Pred. No. 0;
0; Mismatches
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88.4%;
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                                                                                                                                                                                                                                                                                     Sequence 5822
                                                                                                                                                                                                                                disease, and
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 5193;
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Best Local 9
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gene; ss.
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663; Indels DB 20;

Query Match 77.6%; Score 4573.8; Best Local Similarity 87.4%; Pred. No. 0; Matches 5133; Conservative 0; Mismatches

Length 5822; 78;

Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 61 other;

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This is the nucleotide sequence of an isolated nucleic acid which encodes the mouse NaN channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel CDNA was obtained from mouse trigeminal ganglia cDNA by PCR amplification using rat NaN based primers (see AAX87618-19). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAX06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying tissues and cells channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, expression of NaN in censory DRG and frinceminal neurons provides a
                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord.
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P-PSDB; AAY06597.
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4.9	gccgttgcgtgtggccaagccgaataagtttcagtttctagtgatggacttgcccatg 5010
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2y 5071 gg 	ggactccagcggcttggataccatgaaaccatgatggaggagaagtttatggaggcc 5130
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2y 5191 ca 1 0b 5161 ga	aggogocgcogtcatccagaggoctaccggaaacacatggagaagatggtcaaactg 5250
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2y 5783 aaa 5713 aaa	cctaaaagcatgactctgacttgtcagtcagcacccgacttc

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Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena
                                                                                                                                                                                                                                                                                                                                                                                                        Sodium channel; NaN; human; tetrodotoxin resistant; pain;
paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
Location/Qualifiers
31..5402
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                                                                                                                                                                                                                                                                                                                                                         Human sodium channel NaN cDNA.
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P-PSDB; AAB20121.
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dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant production of NaN polypeptides. tetrofotoxin resistant sodium channel, termed NaN (see AAB20121). The CDNA was isolated from a human dorsal root ganglia tissue CDNA library by PCR amplification (see also AAB70122-3). NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in an relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering a agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in The present sequence is that of cDNA encoding a novel human

English.

Claim 1; Fig 11A; 162pp;

Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 other;

DB 22; Length 5860; Score 3242.6; Pred. No. 0; 55.0%; 76.2%; Query Match Best Local Similarity

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agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate production of NaN polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -
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                                                                                                                        Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
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4176 nucleic acids encoding sodium channels, used to develop treating acute or chronic pain or hyperexcitability the nucleotide sequence of a partial cDNA clone which codes ggtctcgtgttcgacatagtcacaagccagatctttgacatcatcatcataagtctcatt gcctttgtgttcgacctggtcacaagccaggtctttgacgtcatcattctgggtcttatt gtcttaaatatgattatcatgatggctgaatctgccgaccagcccaaagatgtgaagaaa acctttgatatcctcaacatagccttcgtggtcatctttaccatagagtgtctcatcaaa ganglia; gene; ss. gtctttgctttgaggcaacactacttcaccaatggctggaacttatttga 4286 sodium channel; ion transport; human; dorsal root paraesthesia; hyperexcitability; therapy; SCN11a This is .rng

contage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and thich produces a TTX-R sodium current. The NaN channel cDNA was obtained from human DRG tissue cDNA by PCR amplification (see also AXA87620-22). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel manA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The named SCN11a 13 gene

Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 1 other;

8 acaaagtttgacaactttggctggtcctttctcgccatgttccgggttatgactcaagac 1110 toctgggagaggetttaccgacagatectgeggacetetgggatetaetttgtettette 1170 accatggettatgaagaacagaacagaaatgtagetgetgagacagaggecaaggagaaa 1290 agaccetgteccaatggttetaegtgegataaaaceaeattgaaceeagacaataattat 1050 816 969 aaggtcatcgtggggggccttgctacgctctgtgaagaagctggtcaacgtgattatcctc 180 tgctttgaaaaagaaagaaaattcacctgaattcaaaatgtgtggcatctggatgggtaac 360 Gaps ttcattgtcattggaacagcgatcgcaacttgttttccggggcagccaagtcaatctttca aaggtcatcgtaggtgccctgctgcgctcggtgaagaagctggtagacgtgatggtcctc aaccagaagtgtattaagcacaactg-----tggccccaaccctgcatccaacaaggat aacctgaaatgcatctcgagggactgtaaaaatatcagtaacccggaagcttatgaccat agtgcctgttccatacaatatgaatgtaagcacaccaaaattaatcctgactataattat ttcgtggtggtcatcttcctgggctccttctacctgcttaacctaacctggctgttgtc Length 3638; Indels 20; 822; DB Mismatches Score 2050.8; No. 0; Pred. .; 0 34.8%; 74.3%; Conservative Similarity Local Simi nes 2756; Query Match Best Loca Matches 1051 1111 1171 1231 661 637 697 61 757 121 181 931 301 991 361 421 481 541 à g ò g 8 G 6 6 6 6 6 6 9 9 9 ò 8 Š 셤

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AAF57009 standard; cDNA; 6344

AAF57009;

ВР

(first entry) 14-MAY-2001

Rat PN3 cDNA sequence.

Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit; tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; rat; sodium channel protein; peripheral nervous system; allodynia; neuropathy; hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerary; analgesic; anti-HIV; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides purified and isolated rat and human peripheral nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins. The rat peripheral nerve sodium channel type 3 (PN3) protein or its human homologue are useful for the development of antibodies against PN3 which are useful in affinity chromatography to purify recombinant sodium channel proteins or polypeptides, or as a research tool. The PN3 proteins are useful as therapeutic targets for compounds to treat disorders of the peripheral nervous system such as allodynia, hyperalgesia, diabetic encopenty, tranmatic injury and acquired immunodeficiency syndrome encoding the rat PN3 protein.
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Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin; modulator; impulse; sensory neuron; acute pain; chronic pain; caaccccatgct------ggaggcaaaagaacactgcaactcctc agccacggaggaggaggaggaccctctgggagagaggacgactttgaaatcttctatgaggt tgcggacgcctgccggagccgttgcgtgtggccaagccgaataagtttcagtttctagt gatggacttgcccatggtgatgggcgaccgcctccattgcatggatgttctctttgcttt gaagtttatggcgaccaatctctccaaagcatcctatgaaccaatagccaccacctccg ctgggagaagtttgaccccgaggcgtcgcagttcatccagtattcggccctctctgactt cgcggacacgctctccggccctcttagaatccccaaacccaaccagaatatattaatcca cogggctgcccgggggaatcaggaccctcctttgctttgatgatgtctcccctctct cDNA encoding variant rat DRG (SNS-B) #3. BP. RESULT 12 AAT77806 JD AAT77806 standard; cDNA; 6527 (first entry) gca 5628 gaa 5237 09-0CT-1997 AAT77806 ు... కిట్టర్లు దీన్లో ఉంది. దీర్వర్లు కిర్మార్లు కిర్మార్లు ఉంది. కిర్మార్లు కిర్మార్లు కిర్మార్లు కిర్మార్లు ఉంది. ఆమార్జులు 20 m

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The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This sequence contains 12 nucleotide differences to the wildtype rat DRG(SNS-B) (see also AAT77803) causing nine amino acid changes.
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                                                  New isolated mammalian sensory neuron sodium channel protein - used to identify modulators of the sodium channel, partic. for the treatment of pain
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                                                                                                                                                                                                                                                                           Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T; 0 other;
                                                                                                  Claim 9; Page 85-93; 128pp; English.
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Matches 3246; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxi modulator; impulse; sensory neuron; acute pain; chronic pain; neuropathic pain; glia; muscle; parasympathetic nervous system; enteric nervous system; central nervous system; dorsal root ganglia;
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The invention provides purified and isolated rat and human peripheral nerve tetrodotoxin (TTX) resistant sodium channel alpha subunit proteins. The rat peripheral nerve sodium channel type 3 (PN3) protein or its human homologue are useful for the development of artibodies against PN3 which channel proteins or polypeptides, or as a research tool. The PN3 proteins are useful as therapeutic targets for compounds to treat disorders of the peripheral nervous system such as allodynia, hyperalgesia, diabetic neuropathy, traumatic injury and acquired immunodeficiency syndrome encoding the human hPN3 protein.
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Qy Db	2598	gccaaagccaaaagagacaacagaaagctttgctggtgagaataaa 2643
Oy Dp	2644	gactcaatcctcccggatgcgaggccctggaaggagtatgatacagacatggctttgtac 2703
Oy Db	2704	actggacaggccggggctccgctggcccactcgcagaggtagaggacgatgtggaatat 2763
Qy Db	2764 3034	tgtggtga
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QY	2974 3274	
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Qy Dp	3388	agtotoatgaatotacoagottgaagtocttocggact 3426 .
ογ	3427	ctgcgggccctgagacctctgcgggcgctgtcccagtttgaaggaatgaaggttgtcgtc 3486

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cardiant; cardioglycoside; pRH3-1; pRH4-23; pRH14-31.
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Sequence Seq

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Title: Perfect score: Sequence:

nucleic

Run on:

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Searched:

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APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Eish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/843,417 FILING DATE: APril 15, 1997 CLASSIFICATION: 536
                                         US-08-455-543A-8
US-08-1293-078B-8
US-08-223-305-8
US-08-149-097D-8
US-08-949-386-8
US-08-455-543A-7
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: 525 University Ave
Palo Alto
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US-08-223-305C-7
US-08-149-097D-7
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US-09-452-007-1
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NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DCOKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6184349
GENERAL INFORMATION:
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TELEFAX: (415)-324-6638
INFORMATION FOR SEQ ID NO: 1:
SEGUIENCE CHARACTERISTICS:
LENGTH: 6344 base pairs
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STRANDEDNESS: single
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Sequence 2,
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3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-08-724-095-7
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Peripheral nerve

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Sequence 1, Sequence 3, Sequence 2, Sequence 3,

US-08-605-284B-21 US-08-605-284B-1

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ORIGINAL SOURCE:

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5445 5114 5174

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APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
                                                                                               5175 gaggaaggaggagcaaggcgccgccgtcatccagaggcctaccggaaacacatgga
                             gatggacttgcccatggtgatgggcgaccgcctccattgcatggatgttcttttgcttt
                                          5386 GATGGACCTGCCGTTGGTCCCCGGGGGATAAGATCCACTGTCTGGACATCCTTTTTGCCTT
                                                                                                                                     gaagtttatggaggccaacccttttaagaagctctacgagcccatagtcaccaccaa
                                                                                                                                                   5506 GAAGITTATGGCGACCAATCTCTCCAAAGCATCCTATGAACCAATAGCCACCACCACCGCGG
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Pred. No. 0;
0; Mismatches 1926;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
                                                                                                                                                                                                                                                                                                                                                                                               Delgado, Stephen G
Fish, Linda M
Sangameswaran, Lakshmi
                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 2834
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 University Ave
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57.3%;
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TELEFAX: (415)-324-0638
INPERATION FOR SEO 1D 0: 9:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Best Local Similarity 57.3
Matches 3227; Conservative
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gaagatgtcaatctcccagccggcccaagttgagaaattactaaggtgtaccgataat 3267 CAGGCCCCTGCTGAGGGAGTGGACGACACAAGCTCCTCTGAGGGCAGCACGGTGGACTGC 3273 aacgggacagacataaa-------tatgtatttggattttaccgaagttccg 3651 CTAGATCCTGAGGAAATCCTGAGGAAGATCCCTGAGCTGGCAGATGACCTGGAAGCA gatagatgettteeceaagggeettagttgteaetttetatgeeaeaaaeagaeaaga agtotoa------tgaatctaccaagottgaagtcttcggact ----ctgaatgatatctttagaaatttacagaaaacagtttcccccaaaaagcagcca tacgccctgatcagcgccatacctgccattctcaatgtcttgctggtctgcctcattttc atcatgaatgctgctgtcgattccagagagaaagacgagccggactttgaggcgaac දැන් යන්නේ නියුත්තයන් නියුත්තයන් නියුත්තයන් නියුත්තයන් නියුත්තයන් නියුත්තයන් නියුත්තයන් නියුත්තයන් නියුත්තයන් Oy da da Óy Q.

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224a-1.rni Page 9	9.428 TACTOTAGETICGEOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	Query Match 19.8%; Score 1168.4; DB 3; Length 6007;
Wed Feb 27 09:58:36 2002	131 APTICANCATCAGGCTCCTICATOCOCCOCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	4915 tattcggcctctctgactttgcggacgccctgccggagccgttgcgtgtggccaagccg 4974

3164 AGAAGGCCAACTGCCAACCACCACGGGGGTGGATATCCACCGGAACGGCGACTTCC 2692 atggctttgtacactggacagggctccgctggcccactcgcagaggtagaggac 1324 AGAAGAACGGAACCACACCACCACCACCACCACCACCACC	2872 gaaatggaagtatttctgaagaagatctgcatttaagcatacagagtcctcgaaagaag	Cy 2992 aatttacagaaacagttcccccaaaaagcagccagatagat	3112 aacatteggaaaacctgctaccaaategtgaagcactggtttgagagtttcataate 3171 1		 Ày 3292 gaaatgatcctgaagtgggtggcctttggattccggaggtatttcaccagtgcctggtgc 3351 	Db 3841 TGGTTGGACTTCCTCATTGTGGCTCTCTTTAGTCAGCCTTATAGCTAATGCCTGGGC 3900 Oy 3396gaatctaccaagcttgaagtccttccggactctgcgggccctgagaccttgggg 3450	gcgctgtcccagtttgaaggaatgaaggttgtcgtctacgccctgatcagcgccatacct	3571 4081	Oy 3616 gacataaatutgtatttggattttaccgaagttccgaaccgaa
Best Local Similarity 60.3%; Pred. No. 8.2e-295; Matches 2225; Conservative 0; Mismatches 1346; Indels 119; Gaps 13; Qy 1616 tettaaccatcacatacaggaacaagaaaattccaggagcttgttcccatgtggga 1675	Qy 1796 tcatcaataccgttttcttagccgtggagcaccacaacatgatgacaacttaaagacca 1855	Oy 1916 teategegetegacettaceactacteceggeaeggetggaatgttttgacagcateg 1975	2036 tcttggcttccctcagagtgctgagggtcttcaagttagccaaatcctggcccagttaa	Oy 2096 acartctattaggatcatcggccactcggtggcgcttggaaacctgactgtggtcc 2155 11 1 1 1 1 1 1 1 1 1	taatt CGACT catgt	2810 TCTTCCACTCCTTCCTTCCGAGTGCTGTGGGGGGGGGGACCGAGTGCTGTGCGGGACCGAGTGCTGTGGGGACCGAGTGCTGTGGGGGGGG	cttca CTTCA gctag	Db 2987 GCGCAGACATGCCGCCACAGACGACGGGGAAATGAACAACTGGAGTCT 3043 Qy 2513 ccctggatcggttccgccgggccttcatgctgcacgctcttca-gagttttgt 2571 Db 3044 CAGTGATCAAGATCAAGAAGGCGTGGACCAAAGTGAAGGTGAAGGTGAAGGTCAAGGTCAAGGTGAAG	ttgct TGAGA cagac

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reco SS: PAULINE CLARK VIEW AVENUE, MS A2-250 atggagaagatggtc 5244 NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REPRENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (550) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 7: ATA: R: US 60/039,447 FEB-1997 DRMATION: US/09024020B STEPHEN G. NDA M.

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                                                                                Score 1168.4; DB 3;
Pred. No. 8.6e-295;
); Mismatches 1346; I
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SEQUENCE CHARACTERISTICS:
LENGTH: 6556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-024-020B-7
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PLICANT: FISH, LINDA M.
PLICANT: HERMAN, RONALD C.
PLICANT: SANGAMESWARAN, LAKSHMI
TLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT
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ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
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AADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
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DIETRICH, PAUL S.
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RAL INFORMATION:
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                                                                                                                                                                                                         Score 1168.4; DB 3;
Pred. No. 8.6e-295;
0; Mismatches 1346;
                                            REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
   APPLICATION NUMBER: US 60/039,447 FILING DATE: 26-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                         Query Match
Best Local Similarity 60.3%;
Matches 2225; Conservative
                                                                                                                    LENGTH: 6586 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                   NAME: CLARK, JANET P. REGISTRATION NUMBER:
                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                           US-09-024-020B-43
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ICANT: SANGAMESWARN, LAKSHMI
E OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
E OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
ER OF SEQUENCES: 43
ESPRONDENCE ADDRESS:
ESPRONDENCE ADDRESSE:
DRESSSEE: JANET PAULINE CLARK
REET: 3401 HILLVIEW AVENUE, MS A2-250 4635 5034 5844 5244 5364 4734 5424 4974 5664 5724 cccatagtcaccaccaccaagaggaaggaaggaggaggaggcaaggcgccgtcatccagagg 5214 atgaaaaccatgatggaggagaagtttatggaggccaacccttttaagaagctctacgag 5154 --ggca 4674 aaagaacactgcaactcctcctcccaagacagctgtcagcagccgcagatagccgtcgtc AAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGATCTTC atcttcaacttcgagacctttacgggcagcatgctgtgcctcttccagataaccacttcg tattcggccctctctgactttgcggacgcctgccggagccgttgcgtgtggccaagccg getggetgggataccetecteaaccccatgetgga-B, Application US/09024020B No. 6030810 DELGADO, STEPHEN G. DIETRICH, PAUL S. FISH, LINDA M. HERMAN, RONALD C. COUNTRY: U.S.A. ZIP: 94304-1397 020B-8 CANT: CANT:

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3295 TCTGACTTCGAGAACCTCAACACAGAGGATG----TTAGCAGCGAATCAGACCCTGAAG 3349
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6826
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1156.8; DB 3;
Pred. No. 9.4e-292;
); Mismatches 1342;
                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
FILING DATE: 26-FEB-1997
ATTORNEY-AGENT INFORMATION:
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHAX: (650) 85-5327
INFORMATION FOR SEC 1D NO: 8:
                                                                                         APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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US-09-024-020B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                           19.6%;
60.2%;
                                                                                                                                                                                                                                                                                                                    LENGTH: 6826 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.2
Matches 2211; Conservative
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                          FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                KESSLER, GOLDSTEIN & FOX I
ork Ave., N. W., Suite 600
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: 08/334,029
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPALIAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
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                                                                ADDRESSEE: STERNE, KESSLER, STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 09:
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
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                                                                                                                COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
              INVENTION: INVENTION:
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cgtggttctttctatcattagtaccctggtttcccgcttggaggacagtgacat.ttctt AGTGATCCTCTCCA----TTGTAGGAATGTTTCTCGCTGAGATGATAGAGAAGTATTTCG GAAGAAGCTTGGGTCCAAAAAACCACAAAACCAATTCCAAGGCCAGGGAACAAATTCCA ATGCCTCAACATGGTAACCATGATGGTAGAAAAAGAGGGGCAAACTGAGTAACATGATTA agtotttgctttgaggcaacactacttcaccaatggctggaacttatttgattgtgtggt GCTAATCTCCCTCAGACATTACTACTTCACTGGGTTGGAACATTTTTGATTTTGGGGT tgtcttaaatatgattatcatgatggctgaatctgccgaccagcccaaagatgtgaagaa aacctttgatatcctcaacatagccttcgtggtcatctttaccatagagtgtctcatcaa ------ggcaaaagaacactgcaact tcaaccccatgctgga-------ವಿಧ್ಯಪ್ರಕಾಣ ಚಿತ್ರಕ್ಷಣೆ ಚಿತ್ರಕ್ಷಣೆ ಚಿತ್ರಕ್ಷಣೆ ಚಿತ್ರಕ್ಷಣೆ ಚಿತ್ರಕ್ಷಣೆ ಅವರ ಕಿಳ್ಳಕ್ಷಣೆ ಚಿತ್ರಕ್ಕೆ ಕ್ರಿಡ್ ಕಿಳ್ಳಕ್ಷಣೆ ಕ

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APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: Sodium Channels, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Aray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                   5111 aggagaagtttatggaggccaacccttttaagaagctctacgagcccatagtcaccacca 5170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325 FILING DATE: 2-MAY-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1017.6; DB 3;
Pred. No. 1.9e-255;
); Mismatches 1459;
                                                                                                                                                                                                                                                                                                                                                                                                                            1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0917.0240002
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PRIOR APPLICATION DATA:
APPLICATION NIME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     Sequence 13, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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nilarity 57.6%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS:
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-08-836-325-13
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Best Local Simi
Matches 2143;
                                                                                                                                                       RESULT 9
US-08-836-325-13
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                                                                                                                                                                                                             Length 6404;
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Pred. No. 2e-255;
0; Mismatches 1459;
    0917.0240002
 REFERENCE/DOCKET NUMBER: 0917
TELECOMUNICATION INFORMATION:
TELEFAX: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 6404 base, pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                            Query Match 17.3%;
Best Local Similarity 57.6%;
Matches 2143; Conservative
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Patent No. 6110672

GENERAL INFORMATION:

APPLICANT: Mandel, Gail

APPLICANT: Halegoua, Simon

APPLICANT: Borden, Laurence A.

TITLE OF INVENTION: Peripheral Nervous System Specific

TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                              5097
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                                                                                                                                                                                                                                                                                   CGTTCACAGATGGAAGAAAGGTTCATGTCTGCAAAATGTCTTCCTAAAGTGTCCTATGAACCC 5652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/836,325
2-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-836-325-14
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2581 3088	tgcaggaggaaaaactcgccaaagccaaaagagacaacagaaagctttgctggtgag 26 	537 147
2638 3148	aataaagactcaatcctcccggatgcgaggccctggaaggagtatgatacagacatggct 26	597 207
2698 3208	ttgtacactggacaggccggggctccgctggccccactcgcagaggtagaggacgatgtg 27	757 267
2758 3268	gaatattgtggtgaaggcggtgcctacccacctcacaacatagtgctggagttcaggcc 28	317 327
2818 3328	ggtgacctccctccagagaccaagcagctcactagcccggatgaccaaggggttgaaatg 28 	377 360
2878 3361	gaagtatttetgaagaagatetgeatttaageatacagagteetegaaagagtetgae 29 	937 120
2938 3421	gcagtgagcatgctctcggaatgcagcacaattgacctgaatgatctttagaaattta 29 	997 475
2998 3476	cagaaaacagtttccccaaaaagcagccagatagatgctttcccaagggccttagttgt 3	057 531
3058 3532	cactttctatgccacaaaacagacaagagaaagtcccctgggtcctgtggtggaacatt 3	591
3118 3592	cggaaaacctgctaccaaatcgtgaagcacagctggtttgagagtttcataatctttgtt 3 	177 651
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3238	gttgagaaattactaaggtgtaccgataatatttcacatttattt	297 771
3298 3772	atcctgaagtgggtggcctttggattccggaggtatttcaccagtgcctggtgctggctt 3	357 831
3358 3832	<pre>gatttcctcattgtggtgtgtgtgtccagtctcatg</pre>	396 891
3397 3892	<pre>aatctaccaagcttgaagtccttccggactctgcgggccctgagacctctgcgggcgctg 34 </pre>	156 951

caagtggcaacctataagggctggctggaaatcatgaatgctgctgtcgattccagagag |||||| |||||| ||||||| || || || || ||| || || || ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || tttgattgtgtgtggtcgttgttctatcattagtaccctggtttcccgcttggaggac TITION TO THE TOTAL TO THE TOTA tcgtggaaggtcccgcaggtcaactttgacaacgtggggaatgcctatctcgccctgctg teceagitigaaggaatgaaggitgtegtetaegeeetgateagegeeataeetgeeatt --taacattagtaattac CGATGGAAAAACCTGAAACTTTGATAATGTCGGACTTGGTTACCTATCTCTGCTT aaagacgagcagccggactttgaggcgaacctctacgcgtatctctactttgtggttttt atcatcttcggctccttctttaccctgaacctctttatcggtgttattattgacaacttc gagtgteteateaaagtetttgetttgaggeaacaetaetteaceaatggetggaaettā tttaccgaagttccgaaccgaagccaatg-ుడుది. ది. ది..రు. ది..రు. ది..రు. ది..రు. ది..రు. ది..రు. ది. రు. ది..రు. ది..రు

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                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Pred. No. 4.3e-216;
0; Mismatches 758;
                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NO-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NO-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                             APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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ilarity 63.8%;
Conservative
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TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: BORDEN, Laurence A.
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CORRESPONDENCE ADDRESS:
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ttent No. 5858713
ENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
APPLICANT: SOGERUND:
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051 5180 aggaggaggaaggcgccgccgtcatccagaggcctaccg 5222 OPPRATING TYPE PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/808,793 IBM PC compatible COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy New York : USA STREET: Clinton CITY: Rochester STATE: New York tgctgga----ZIP: 14603 LT 12 3-808-793-24 COUNTRY: 4664 2135

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CTCCCCGACGCCTCATCAAGAAGGGGATCAAGGAGCAGAGCAGCACTGGAGCTGCCCATC 3372
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Matches 1923; Conservative
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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t No. 5550049
t No. 5550049
t Nature Marmke, Jeffrey W.
PLICANT: Warmke, Jeffrey W.
PLICANT: Warmke, Jeffrey W.
TLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE MBER OF SOUGHCES: 7
MBER OF SOUGHCES: 7
ADDRESSEE: John W. Wallen III
ADDRESSEE: John W. Wallen III
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MPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
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               Version #1.25
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                                            APPLICATION NUMBER: US/08/338,702
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                   NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19338
TELECOMMUNICATION INFORMATION:
TELEFAX: (908) 594-3905
TELEFAX: (908) 594-305
INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                    11.5%;
52.6%;
                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                           linear
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MOLECULE TYPE:
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Matches 1941;
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US-08-337-339-7
Sequence 7, Application US/08337339
Patent No. 559384
GENERAL INPORMATION:
APPLICANT: Hall, Linda
APPLICANT: Hall, Linda
APPLICANT: Ferg, Gouping
APPLICANT: Ferg, Gouping
APPLICANT: PROFESSION OF THE
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
CORRESPONDENCE NON W Wallen III
STREET: P.O. BOX 2000, 126 E. Lincoln Avenue
                                       ctcttccagataaccacttcggctggctgggataccctcctcaaccccatgctggaggca
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ವಿಶಿವರೇಚಿಸುವರೇಚಿಸು ರು. ಡಿ. ರು.ಚಿ. ಕೇ. ಡಿ. ರೇ.ಶಿ. ಚಿನುರು. ವಿನರ್ವ ಕಿ. ರಕ್ಷ ಶಿಸ್ತರು ಕಿ. ಚಟ್ಟಿಚಿಸು ರುಷಟಿಸಿದ್ದಾರೆ.
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                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 676.6; DB 1;
Pred. No. 2e-166;
); Mismatches 1569;
                                                                                                                                                                            CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III. John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19332
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDINES: single
                                                                                                                   SOFTWAKE: FULLING DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.5%;
52.6%;
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.6
Matches 1941; Conservative
                                                                                                                                                APPLICATION NUMBER:
FILING DATE:
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MOLECULE TYPE: CDNA
US-08-337-339-7
                    RY: USA
07065-0900
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                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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	4255 cactacttcaccaatggctggaacttatttgattgtgtggtggtcgtggttcttctatcatt 4314 	m Salina sa sa sa	Patent No. 5688 GENERAL INFORM APPLICANT: APPLICANT:
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Warnke, Jeffrey W.
Hall, Linda
Feng, Gouping
Van Der Ploeg, Leonardus
WENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE cagaggcctaccggaaacacatggag 5235 oplication US/08724095 8917 MATION:

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Pred. No. 2e-166;
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E. Lincoln
   SODIUM CHANNEL
                                                                                                      COUNTRY: USA

ZIP: 0705-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ: Version #1.d5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,095
                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATORNEY/ACENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 35,545
REFERENCE/DOCKET NUMBER: 19332DA
TELEPHONE: (908) 594-3905
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
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52.6%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 1941; Conservative
                                            ADDRESSEE: J. Mark Har
STREET: P.O. Box 2000
TITLE OF INVENTION: PARTICUMER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                            New Jersey
USA
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US-08-724-095-7
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Search completed: February 26, 2002, 22:39:38 Job time: 17238 sec

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February 26, 2002, 17:49:55 ; Search time 5057.4 Seconds
(without alignments)
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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O	485.4		892	11	BF980111	BF980111 602288113
e	305.4		778	10	AU035605	AU035605 AU035605
4	283.4		615	10	AW133907	AW133907 fil3c05.y
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σ	239.6		610	10	AL588672	AL588672 AL588672
10	236.6		689	11	BF347024	BF347024 602021819
11	236.2		779	10	AU051532	AU051532 AU051532
12	234.2		529	10	AA183990	AA183990 ms53e02 r

BF470392 UI-W-BH3-BG578677 dac36c11. AL290746 Tetracadon BE0198746 Tetracadon BE0198767 maa38e08. AZ438465 1M0228N06 AZ96529 WM0428N06 AZ96529 WM0428N06 AZ965314 1M0331P08 AA913881 am34c11.s AA98321 am34c11.s BG253038 60236566 BG761119 GA211452 BE864903 UI-W-BH1-BH1-BH03847 RPCI-24-3 AZ39295 1M0155L16 AZ01573 RPCI-24-3 AZ39295 1M0155L16 AZ01573 RPCI-24-3 AZ39295 1M0155L16 AZ01573 RPCI-24-3 AZ39295 1M0155L1 MAR AL51795 ML517958 AL51795 WI-SP776 AZ39294 UI-W-BH1-AZ33959 LBH1-AZ33359 BE724185 198931 MA F07776 HSCZHD061 n BE121161 UI-R-CA0-AA46818 XW09604 s BG66779 DRABWE08 AZ39294 BIN155J16 AV721039 AV721039 AV721039 AV721039	PENTS EST 04-MAY-2001 pituitary Mus musculus cDNA clone Ce. Craniata: Vertebrata: Euteleostomi; Sciurognathi: Muridae; Mus. nih.gov/ncicgap. ncer Genome Anatomy Project (CGAP), h.D. Bento Soares Laboratory I.M.A.G.E. Consortium/LLNL Institutes of Health Intramural clone distribution information can be Consortium/LLNL at: mn: 19 lus" 0" MBP2 pituitary"
BF470392 BC578677 BC578677 BC018461 BF323367 AZ438465 AZ438465 AZ438465 AZ438465 AZ438465 AZ495334 AZ495334 AZ495334 AZ495338 AZ495338 AZ495338 AZ495338 AZ41755 AZ41756 AZ41756 AZ41756 AZ4185	mRNA WMBP2 pi sequence cdata; C entia; S l.nlm.ni ce, Canc re, Canc re, Canc re, Canc re, Canc re, Canc column fiers musculu n:10090" al16490" ares NMB
	Soares NMB; ', mRNA seq 13953218 120a; Chorda rria; Rodent 650) '/www.ncbi.n '/www.ncbi.n '/www.ncbi.n '/www.ncbi.n 'rriayed by: 'mstitute,' 'stausberg 'email.nih.gy 'gy) 'mstinn' 'mstinn' 'gy) 'mstinn' 'mstinn
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	BG694370 650 bp NISC_iv01b10.w2 Soares R BG694370 GI:13953218 BG694370.1 GI:13953218 EST. Mus musculus Eukaryota: Metazoa; Chon Mammalia; Eutheria: Rode 1 (Dases 1 to 550) NCI-CGAP http://www.ncb; NCI-CONTA Library Preparation CONTA Library Preparation CONTA Library Arrayed bp DNA Sequencing by: Nat; Sequencing Center (NISC; Clone distribution: NC; Clone distribution: NC; Clone distribution: NC; Clone distribution: NC; NGI:1597258 Plate: LLAM9919 row: C Seq primer: T? primer. Location/Quali; 1. 650 /Crgania="Muscip-Raxof" /Clone="INAGE:"Axof. /Clone="INAGE:"Ax
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602288113T1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4373859 3'
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                                                                                                                                        Score 541.2; DB 11; Length
Pred. No. 3.7e-100;
0; Mismatches 68; Indels
tissue_type="pituitary gland"
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BF980111
BF980111.1 GI:12347326
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/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', Size selected for wherage insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 892)
                                                                                                                                                                                                                                                                Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM10036 row: j column: 04
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), &
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 8.5e-89;
0; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4373859"
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 13
High quality sequence stop: 729.
Location/Qualifiers
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Best Local Similarity 81.7
Matches 609; Conservative
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                        Homo sapiens
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Similarity
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                                    Matches 505;
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                                                                                                                                                                                                                                                                                                                                         AU035605 778 bp mRNA EST 12-JUL-2000 MU53605 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-0634, mRNA sequence.
AU035605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
Construction of mouse full length-enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
gggactgtagccctcagtggctgtgcataaagaaggtcctgcggaccatcatgacggatc 1762
                                                                                                                                                                                                     cetttactgagetggecatcaccatetgcatcatcatcatacataccgttttettageegtgg 1822
                                               CGTTTACTGAGCTGGCCATCACCATCTGCATCATCATCAACACTGTCTTGGCCATGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; E
Sciurognathi; Muridae;
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/clone_lib="Sugano mouse
/sex="female"
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/strain="C57BL"
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/lab_host="TOP10"
                                                                                                                                                                                                                                                                 AGCATCACAAGATGGAGGCCAGGTT
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                                                                                       gtatctctactttgtggtttttatcatcttcggctccttctttaccctgaacctctttat
                                                                                                              4 GTATCTGTACTTTGTCATCATCATCTTTGGGTCGTTCTTCACTCTAAAATCTATTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4380 ccgcttggctcggattggtcgaatcctcaggctggtccggggctgcccggggaatcaggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 GCTGCTCTTTGCTCTGACCATGTCCCTTTCTGCGCTGGTCAACAATCGGGCCTCCTGCTT
                                           12;
                                           248; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 305.4; DB 1 Pred. No. 4.6e-52;
                                           0; Mismatches
5.2%;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio
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/de_stage==dill_file.
/lab_host==DH10B (phage resistant)"
/lab_host==DH10B (phage resistant)"
/note==Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCANGTG): 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor!
[TGTTGGCCTAGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the CDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Kolchi Kawakami. Custom primers for
sequenocing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCAGCAC.

stage of the pME18S-FL3 vector.

sequenocing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCAGCAC.

stage of the pME18S-FL3 vector.

stage of the pME18S-FL3 vector.

sequenocing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCAGCAC.

stage of the pME18S-FL3 vector.

stage of the pME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugano and Dr. Koichi Kawakami DNA
ity Genome Sequencing Center
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1 (bases 1 to 615)
Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S.,
Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,Š., Kucaba,T.,
Martin,J., Pape,T., Steptoe,M., Underwood,K., Theising,B., Ritter
'E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GGCCGCTGCGTGAACCGGACGGGTTTCATCTATAATTCCTCTGACATCAACAACCGCAGC 121
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including
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Pred. No. 1.5e-47;
0; Mismatches 196; Indels 3;
                                                                                                                                                                                                                                                                            Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
11: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="2601032"
/clone_lib="Sugano Kawakami zebrafish
/sex="mixed (one male and one female,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Suga
Sequencing by: Washington University
Seq primer: T3 ET from Amersham
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unfertilized eggs)"
                                                                                                                                                                                                                   Unpublished (1999)
Other_ESTs: fill3c05.x1
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ilarity 67.5%;
Conservative C
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ORIGIN
                                                                                                                                                                               TITLE
JOURNAL
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   REFERENCE
                                       AUTHORS
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                                                                                                                                                                                                                                                   COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. I (bases 1 to 67).

NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cloue_lib="NHL_MGC_94"
/tissue_type="retina"
/tasue_type="retina"
/tasue_type="retina"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3: 3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                 BG342331 674 bp mRNA EST 27-FEB-2001 602374246Fl NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4061 ttgtgttcgacctggtcacaagccaggtctttgacgtcatcattctgggtcttattgtct 4120
                                                                           4011
4012 aagaaacctcaaaaagcccatcccaaggcccctgaacaaatgtcaagcctttgtgttcgac 4071
                                                                                                                                                                                                                           4072 ctggtcacaagccaggtctttgacgtcatcattctgggtcttattgtcttaaatatgatt 4131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL) DNA. Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TGGTTTTTGACTTTGTAACCAGACAAGTGTTTGATATCAGCATCATGATCTCTGTC 64
                                                                                                                                                                        gacatttttatgacagaagaacagaagaaatattacaatgcaatgaaaaagttaggaacc
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Pred. No. 3.9e-44;
0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10317 row: 1 column: 12
High quality sequence stop: 672.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:4481819"
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                                                                                                                                                                                                                                                                                                   4132 atcatgatggctg 4144
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                                                                                                                                                                                                                                                                                                                                        602 ACGATGGATGGTG 614
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ORIGIN
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TITLE
JOURNAL
                                                                             3952
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KEYWORDS
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NcI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCA-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l (bases 1 to 561)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laggreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Llang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                  /db_xxef="taxon:9606"
/clone="IMAGE:3220170"
/clone_lib="NCI_CGAP_GG6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 255.4; DB 10;
80.8%; Pred. No. 7.5e-42;
tive 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                        199
   Location/Qualifiers
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                                     /organism="Homo
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE550573 690 bp mRNA EST 10-AUG-2000 7a29e10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3220170 3' similar to TR:088457 088457 VOLTAGE-GATED NA CHANNEL ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 690)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                      4420
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Seq primer: -400P from Gibco
High quality sequence stop: 456.
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BE550573
BE550573.1 GI:9792265
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EST

VERSION KEYWORDS SOURCE ORGANISM

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AUTHORS TITLE

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25-APR-2001

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                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 247.8; DB 11; Length 561;
Pred. No. 2.8e-40;
0; Mismatches 187; Indels 3;
Libraries and construction of a gene index for Genome Res. 11 (4), 626-630 (2001)
                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                           adrenal, and endometrium.
                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC_2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                  Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                   BACKWARD: GTTTCCCAGTCACGACG
Plate: 86 row: H column: 12
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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PCR PRimers
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                                                            Contact: Smith TPL
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Matches 373; Conservative
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1 (bases 1 to 619)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CBIO 1SB. Email: biohelp@Hymp.mrc.ac.uk
                                                                                                                            GSS 27-FEB-1997
010M03aE5, genomic survey sequence.
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Location/Qualifiers
1. .619
/ craganism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 010M03"
/clone="010M03aE5"
/clone="010M03aE5"
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Pred. No. 2.4e-39;
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                                                                                                                            FR0002753 619 bp DNA
F.rubripes GSS sequence, clone
286536
                                                                                                                                                                                                                GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
TCATCTATGCCATCTTTGGAATG 560
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al Similarity 68.5%;
335; Conservative
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PRIMER: M13
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/note-"Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF347024 689 bp mRNA EST 22-NOV-2000 602021819F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157189
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                  4335 ggaggacagtgacatttctttcccgcccacgctcttcagagtcgtccgcttggctcggat 4394
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                                                                                              301 GAACATCTTTGACTTCGTTGTTGTGATTCTGTCCATTGTGGGAATGTTCCTGGCTGAAAT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 689)
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http://image.llnl.gov
Plate: LLAM9431 row: f column: 06
High quality sequence start: 3
High quality sequence stop: 654.
Location/Qualifiers
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/clone="IMAGE:4157189"
/clone_lib="NCI_CGAP_Brn67"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: frazér.murray@bbsrc.ac.uk
GCGCCCCGCTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
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AL588672 BP Chicken Brain Library Gallus gallus cDNA clone
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tive 0; Mismatches 216; Indels 4;
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/db_xref="taxon:9031"
/clone="ROS075G04"
/clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP Chicken Brain Library
Unpublished (2001)
Context: Frazer Murray
Dept. Genomics and Bloinformatics
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Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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1. .610
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us-09-646-224a

DB 11; Length 689;

Score 236.6;

Query Match

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Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
Construction of mouse full length-enriched cDNA libraries by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU051532 779 bp mRNA EST 12-JUL-2000 AU051532 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-215151, mRNA sequence.
AU051532
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                                                      3356 ttgatttcctcattgtggtggtgtctgtgctcagtctcatgaatctaccaagcttgaagt 3415
                                                                                                              ccttccggactctgcgggccctgagacctctgcgggcgctgtcccagtttgaaggaatga 3475
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                               Gaps
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Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashienidenid.go.jp
URL: http://www.nih.go.jp/yoken/genbank/
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
I (bases 1 to 779)
                              Indels
              Pred. No. 5.1e-38;
; Mismatches 214;
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Contact: Katsuyuki Hashimoto
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/de_stage="adult"
//de_lost="adult"
//de_lost="TOP10"
//de_oragin="adult"
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Seq primer: 5' end primer: CTTCTGCTCTAAAAGCTGCG
POLYA=No.
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Pred. No. 6e-38;
0; Mismatches 192;
                                                                                                                                                                                                                                                                                                             /clone="MNCb-2151"
/clone_lib="Sugano mouse
                                                                                                                                                    1. 7/9//organism="Mus musculus"
                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                        /strain="C57BL"
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Best Local Similarity 65.7%;
Matches 371; Conservative
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 529)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                     ms53e02.rl Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cobn clone ImAGE:615290 5' sinilar to 9b.M81758 SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); 9b:U26707 Mus musculus voltage-gated sodium channel alpha subunit SCNBA (MOUSE);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortlum (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4171 aagaaaacctttgatatcctcaacatagccttcgtggtcatctttaccatagagtgtctc 4230
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/clone="IMAGE:615290"
/clone=lib="Life Tech mouse embryo 13 5dpc 10666014"
/taxoue_type="embryo"
/dev_stage="13.5dpc embryos"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 529;
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High quality sequence stop: 263.
Location/Qualifiers
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                                                                mRNA
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                                                             529 bp
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Fax: 314 286 1810
                                                                                                                                                                                                             mRNA sequence.
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/clone_lib="University of the process of the modified normalized libraries from tensor of the modified polylinker; Site_l: Not I: Site_2: Eco RI; The lolylinker; Site_1: Site_2: 
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMMP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMMP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 547)
Bonaldo, M. E., Lennon, G. and Soares, M. B.
Normalization and subtraction: two approaches to facilitate gene
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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Fax: 301 443 9890
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NIH_BWAP_M_S2; NIH_BWAP_M_S1. The subtracted library (NIH_BWAP_M_S4) was constructed as follows: PcRamplified cDNA inserts from NIH_BWAP_M_S3.3, NIH_BWAP_M_S3.2, and NIH_BWAP_M_S3.1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with a pool of the NIH_BWAP_M_S3.3, NIH_BWAP_M_S3.2, and NIH_BWAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (LifeTechnologies) to generate the NIH_BWAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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                                                                                                                                                                                                                                                                                                                                           Length 547;
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Xenopodinae; Xenopus. 1 (bases 1 to 518)

REFERENCE

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Email: est@watson.wustl.edu
Library constructed by Life Technologies. DNA Sequencing by:
Library constructed by Life Technologies. DNA Sequencing by:
Washington University Genome Sequencing Center.
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINE at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stope: 392.
Lioration/Qualifiers
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
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/clone="lMAGE:4409085"
/clone=lib="NICHD XGC Hel"
/lab_lost="blost="HIOB (phage-resistant)"
/note="organ: heart; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:6 kb. Constructed by Life
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                                                                                                                                 Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Pred. No. 6.5e-36;
0; Mismatches 171;
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                                                                                       WashU Xenopus EST project, 1999
Unpublished (1999)
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174 TGATCTCCAKGGACMTGCCMATGCTMAGTGGGGAMAAGATMMACTGCCTGGACATMATCT
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                                                                                         26, 2002, 20:07:03
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ne: 8228 sec
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Job time
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
qenome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                          Tetraodontidae; Tetraodon.

1 (bases 1 to 501)

1 (Scost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Westsenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                      Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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/organism="Tetraodon nigroviridis"
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/clone="110m19"
/clone=11b="G"
/note="Genoscope sequence ID : COBG110AG10LP1-end"
/note="Genoscope sequence ID : COBG110AG10LP1-end"
- 133 c 116 g 133 t 25 others
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67.2%; Pred. No. 9.1e-35;
iive 15; Mismatches 138; Indels
                                                                                                                                                        GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Best Local S
                               CNSO4HC1/c
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DEFINITION
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OM protein - protein search, using sw model

February 26, 2002, 22:39:30 Run on:

; Search time 76.96 Seconds
(without alignments)
1698.796 Million cell updates/sec

US-09-646-224A-2 9173 1 MEERYYPVIFFDERNFRPFT.....VFCNGDLSSLDVAKVKVHND 1765 Title: Perfect score: Sequence:

BLOSUM62 Capoxt 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDS_/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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/SIDS2/gcgdata/geneseg/genesegp/AA2001

SUMMARIES

	Description	Rat sensory neuron	Type 5 sodium chan	Rat sodium channel	Rat sodium channel	Rat sodium channel	Mouse sodium chann	Mouse sodium chann	Human sodium chann	Human hH1 sodium c	Human SCN5A mutant	Human SCN5A protei
	ID		AAY16572	AAY06596	AAB20122	AAB20123	AAY06597	AAB20124	AAB20121	AAW23994	AAB82242	AAB82239
	DB	20	20	20	22	22	20	22	22	19	22	22
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	Score	9173	9153	9149	9149	9141	8153	8153	6109	4712.5	4712	4711.5
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ALIGNMENTS

Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity. Rat sensory neurone specific 2a protein sequence. NAY41668 TD AAY41668 standard; Protein; 1765 AA (first entry) 03-DEC-1999 AAY41668; RESULT

99WO-GB00838. W09947670-A1 18-MAR-1999; 23-SEP-1999 Rattus sp.

Tate SN; 98GB-0005793. (GLAX) GLAXO GROUP LTD. Grose DT, Hick CA, 18-MAR-1998;

WPI; 1999-562112/47. N-PSDB; AAZ21480.

Mammalian sodium channel protein for treating pain and hypersensitivity

Claim 1; Page 59-64; 73pp; English.

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                                                                     The present sequence represents rat sensory neurone specific 2a (SNS-2a) SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a type 5 sodium channel protein designated PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root gangila. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and
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Pred. No. 0;
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                                                                                             neuropathic
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diabetic
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	Region 10981117 Alabel	Region 1	Alabel	Tr. /note= "domain IV transmembrane segment 56" X	N WPI; 1999-479168/40. N N-PSDB; AAX87600. N New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability. T phenomena
				EX8X6X5X5X5X5X5X5X5X5X5X5X5X5X5X5X5X5X5X5	
VVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQF 1620	T 3 596 AAY06596 standard; Protein; 1765 AA. AAX06596; 26-OCT-1999 (first entry) Rat sodium channel NaN.	odium channel; ion transport; rat; dorsal root gang paraesthesia; hyperexcitability; therapy. sp. Location/Qualifiers 125148 /label= DI-S1 /note="domain I transmembrane segment S1 157177 /label= DI-S2		353.358 /label= DI-SS2 /note= "domain I transmembrane segment SS2, the Ser-355 residue is implicated in the TTX-R phenotype" 771.398 /label= DI-S6 /note= "domain I transmembrane segment S6" 567.591 /label= DII-S1 /note= "domain II transmembrane segment S1" 603.624 /label= DII-S2 /note= "domain II transmembrane segment S2" 603.624 /label= DII-S2 /note= "domain II transmembrane segment S2" 633.654	
1561 v 1561 v 1621 i 1621 i 1681 Di 1681 Di 1741 St	RESULT 3 AAY06596 ID AAX06596 st. XX AC AAY06596; XX	NaN; Sc pain; B Rattus Key Region Region	Region Region Region	Region Region Region Region	Region
60	RESU AAYO ID XX AC XX DT XX	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX			FTT

This is the predicted amino acid sequence of the rat NaN channel, as deduced from isolated rat NaN CDNA (see AAX87600). NaN is a previously unidentified voltage gated sodium channel protein that is previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The impose and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAX87600-02) and polypeptides (see AAX87600-02) and polypeptides (see AAX87600-02) and collypeptides expression vectors and transformed host cells, methods for identifying spanets that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and spensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. 91pp; English 2A-C; 1; $\overset{\pi}{\times}\overset{\circ}{\times}\overset{\circ}{\circ}{\circ}\overset{\circ}$

AA; 1765 Sequence

ö 240 360 480 480 540 540 180 300 360 420 420 9 009 999 120 9 9 ROILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEDONRNVAAETEAKEKWFOEAO **MEERYYPVIFPDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASR** LMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGF IVDEFSFLRDPWNWLDFIVIGTALATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIV GALLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASNKDCFEKEK DSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLY KTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDNN RSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGT ö Length 1765; Indels 20; 5 DB Score 9149; DE Pred. No. 0; 4; Mismatches 99.78; Conservative Best Local Similarity Matches 1759; Conser Query Match Best Local 3 ч 61 121 181 241 361 541 61 121 241 301 301 361 421 421 481 481 601 661 g õ g g οy g Sy D Oy q ò g Q Dp oy D ô g ò g ò ò ò

1741

720

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g

1380 1560 1020 1140 1140 840 780 840 900 900 960 960 WNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFL LEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLMNLPSLKSFRTLRALRPLRALSOFE DDVEYCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRK KSDAVSMLSECSTIDLNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLW GMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEV PNRSQCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEA TKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDI LNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTL FRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSWFSK VVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQF 1QYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGL **DTMKTMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHMEKMVKLRLKDR\$** IMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSF SSSHQVFCNGDLSSLDVAKVKVHND 1765 ssshqvfcngdlssldvakvkvhnd 1765 1141 1441 1081 1141 1321 1381 1441 1621. 1741 1021 1021 1081 1201 1201 1261 1321 1501 1561 1621 1681 721 781 781 841 841 961 1261 1381 1501 1561 1681 721 901 901 961

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                                                                                                                                                                                              /note= "transmembrane domain DI-SS2, includes residue at position 355 implicated in tetrodotoxin resistance"
                                                                Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
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263..1288
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                                                                                                                                                                                                                                                                                                                              "transmembrane domain DII-SS2"
                                                                                                                                                                                                                                                                                                                                                          note= "transmembrane domain DIII-S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "transmembrane domain DIII-S6"
                                                                                                                                                                                 'note= "transmembrane domain DI-SS1"
                                                                                                                                                                                                                                                                                                                                                                       note= "transmembrane domain DIII-S2"
                                                                                                                                                                                                                                                                                                                                           "transmembrane domain DII-S6"
                                                                                                                                                                                                                                                                                                 "transmembrane domain DII-S5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "transmembrane domain DIV-S4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "transmembrane domain DIV-S5"
1513..1527
                                                                                                                                                                                                                                        "transmembrane domain DII-S1"
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.e= "transmembrane domain
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      AAB20122 standard; Protein; 1765 AA.
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125..148
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029..1052
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                                   30-APR-2001 (first entry)
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699..719
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AAB20122
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The present sequence is that of novel rat tetrodotoxin resistant sodium channel NaN, as deduced from CDNA (see AAF30102) isolated from a rat dorsal root ganglia tissue library. The sequence shows 69% similarity to human NaN (see AAB20121). NaN belongs to the a-subunit voltage-gated sodium channel protein family. It produces a TYX R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an expense that alters sodium current flow through NaN channels, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which modulates transcription or translation of Nan MRNA, in dorsal root ganglia or trigeminal neurons. Nan polypeptides can be obtained by recombinant expression, and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate sodium channel expression or activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                   /note="transmembrane domain.DIV-SS2"
1558.1584
/note="transmembrane Arms:" """
/note= "transmembrane domain DIV-SS1"
1529..1534
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Pred. No. 0;
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Q	541 cgknlaskylvwdcspgwlcikkvlrtimtdpftelaiticiiintvflavehhnmddhl 600			681
yo g	KTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDNN 66			1681 dtmktmr
2 2	KILIKIGOMWILGILIGEMCIKLIGIQPYNYIENGWNVEGSIVALISIAQVIYNELSGUN 66		Öy 1	1741 SSSHQVI
g 8	ooi Kstabakvikrikuksykriniitiitiiliiliiliiliiliiliiliiliiliiliili			1741 ssshqv
Oy .	721 KENKTAYATOERPREMHMDNEYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVL 78		RESULT 5	
දු	721 kfnktayatqerprrrwhmdnfyhsflvvfrilcgewienmwgcmqdmdgsplciivfvl 78			17
dy Op	/81 IMVICKLVUNLEIALLNEFSDEEKSCS-ERGETRYRYVOOLALDERREFSFEHLALOSF 840			AAB20123; 30-APR-2001
δy	841 CCKKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDWALYTGQAGAPLABVE			Rat sodium o
q	841 C			Sodium chann paraesthesia
oy d	901 DDVEYCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSTQSPRK 960			diagnosis.
ìò	961 KSDAVSMESECSTIDENDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLW 10			Domain
d d				·- ·
οy	1021 WNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFL 10			Domain Domain
g ,	1021 wnirktcygivkhswfesfiifvillssgalifedvnlpsrpqvekllrctdniftfifl 108			Domain
oy B	1081 LEMIKKWARGERRYETSANGWLDFLIVVVSVLSLMNLPSIKSFRTLRALRPLRALSGFE 1140 1081 lemilkwvafgfrryftsavovlaldflivvvsvlslmnlpsiksfrtlralrplralsgfe 1140			Domain
δy	1141 GMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEV 12			Domain
q				
oy G	1201 PNRSQCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEOPDFEA 1260			Domain
ò	1261 NLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNOOOKKIGGODIFWTEEOKKYXNAMKKIG 13		FF	Domain
d d				Domain
				Domain

Jo	1321	TKKPQKPIPR	PQKPIPRPLNKCQAFVFDLVT 	FDLVTSQVFDV 	IILGLIVLN 	MIIMMAESA 	SQVFDVIILGLIVLNMINMAESADQPKDVKKTFD 	FDI 1	380
- G G	1381	LNIAFVVIFT 	TECLIKVEA	IKVFALRQHYFTNGWNLFDCVVVVLS 	LFDCVVVVI 	SIISTLVSRLE	LEDSDISFP	3	1440
Ş.cq.	1441	FRVVRLARIG 	IGRILRLVRAARGI 	RGIRTLLFALM rgirtllfalm	MSLPSLFNJ mslpslfnj	IRTLLFALMMSLPSLFNIGLLFLYUMFIYA 	'IYAIFGMSWFE 	×-×	1500
	1501	VKKGSGIDDI vkkgsgiddi	FNFETFTC fnfetftg	SMLCLFQITTSA 	GWDTLLNPN gwdtllnpn	ITTSAGWDTLLNPMLEAKEHCNS. 	Post of the state	4 – e	156(156(
.;&. qa	1561	VVYEVSYIII 	SFLIVVNMYIAVII 	IAVILENFNTA	TEESEDPLC teesedplg	EDDFEIFYE eddfeifye	LENFNTATEESEDPLGEDDFEIFYEVWEKFDPEA: 	SQF III	162(162(
oy d	1621	ALSD 	ADALPEPLRV 	FADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDS: 	DLPMVMGDE dlpmvmgdı	<pre>LHCMDVLFA hcmdvlfa</pre>	FTTRVLGDS 	SGL	168(168(
. 65 . da	1681	DTMKTMMEEK 	KEMEANPEKK 	DTMKTMMEEKFMEANPFKKLYEPIVTTKRKEEEQGAAVIQRAYRKHMEKMVKLRLKDRS 	KEEEQGAAV 	/IQRAYRKHW 	EKMVKLRLK 		174(174(
	1741	SSSHQVFCNGDLSS 	3DLSSLDVAK dlssldvak	SSLDVAKVKVHND 1765 ssldvakvkvhnd 1765					
KEST AAB	23 AB2	5 0123 standa	ard; Prote	ein; 1765 AA					
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X E	-	APR-2001 (f	first entr	ry)					
X E X	T.	sodium channel	nnel NaN.						
K K K K K K K K K K K K K K K K K K K	odi ra Lag	um channel; esthesia; h nosis.	; NaN; rat hyperexcita	; tetrodoto ability; an	xin resi algesic;	stant; pai vaccine;	.n; therapy;		
XES	Key	<u>.</u>	Location	/Qualifiers					
	Domain	<u> </u>	/note= "	transmembra	ne domai	n DI-S1"			
E E	Domain	e. :	/note= "	transmembra	ne domai	n DI-S2"			
г., т.	Domain	Ľn	/note= " 216237	transmembra	e domai	DI-S3			
H H .	Domain	rn	/note= " 254273	transmembra	e domai	DI-S4			
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1 E E			וסרפ. ייסור	residue at p	e domai osition resist	n D1-332, 355 impli ance"	cated in	מ ת	
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	Domain		033054 /note= "tra .663682	transmembrane	ne domain	DII-S3"			

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The present sequence is that of novel rat tetrodotoxin resistant sodium channel NaN, as deduced from cDNA (see AAP30102) isolated from a rat dorsal root ganglia tissue library. The sequence shows 69% similarity to human NaN (see AAB20121). NaN belongs to the a-subunit voltage-gated sodium channel protein family. It produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human tetrodotoxin resistant schannels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena
                                                                                                                                                                                                                                                     note= "transmembrane domain DIII-SS1"
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                                                                                                                                                             DIII-S3"
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                                                                  "transmembrane domain DII-SS2'
note= "transmembrane domain DII-S4"
                                                                                         "transmembrane domain DII-S6"
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the face (trigominal gangia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in be obtained by recombinant expression, and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate sodium channel expression, to screen for and to raise antibodies useful as diagnostic agents. ~ DO DO DO DO DO DO X O ...

1765 AA Sequence

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                                                                                                                                                             RQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEBONRNVAAETEAKEKMFQEAO
                                                                                                                                                                                                                                                                                                                                                                                                           61 KLPKLYGDIPPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRS
                                                                                                                                                 LMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGF
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                                                 MEERYYPVIFPDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASR
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                         0;
  Length 1765;
                         Indels
  DB 22;
                        3; Mismatches
 Score 9141;
Pred. No. 0;
99.78;
 Query Match 99.7
Best Local Similarity 99.6
Matches 1758; Conservative
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sodium

AC AAY06597; XX XX DT 26-0CT-1999 (first entrv)	Mouse	pain; paraesthesia; hyperexcitability; therapy. Mus musculus.	Key Location/Qualifiers Region 125148 (label= DI-S1	Region / 159179 / 1891on /	/label= DI-S3 /note= "domain I transmembrane segment 21924 /label= DI-S4	Region	Region Region		Region Region	/label= Dil-52 /note= "domain II transmembrane segment Region 636.657 /label= DII-53	Region	FT Region 701720 FT /label= DII-S5 FT /note= "domain II transmembrane segment S5" FT Region 743.751		FT /note= "domain II transmembrane segment SS2" FT Region 775800 FT /label= DII-S6 FT /note= "domain II transmembrane segment S6"	Region 10311053 /Jabel= DIII-S1 /note= "domain III transmembrane Region 10681093		Region //10.1140 //10.1140 //10.1140 //10.1140 //10.1140 //10.1140 //10.1180
781 IMVIGKLVVLNLFTALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSF 840	ALYTGO	DDVEYCGEGGALPTSOHSAGVOAGDLPPETKQLTSPDDGOVEMEVFSEEDLHLSIQSPRK	HFLC	WNIRKTCYQIVKHSWFESFIIEVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIEL	LEMILKWYSEGFRYFFTSAWCMLDFLIVVVSVLSLMNLPSLKSFRTLRALRPLRALSOFE LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACINGTDINMYLDFTEV	1201 PNRSQCNISNYSWKVPQVNFDNVGNAYLALLGVATYKGWLEIMNAAVDSREKDEQPDFEA 1260 	1261 NLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQOKKLGGQDIFWTEEQKKYYNAMKKLG 1320 	1321 TKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIINMAESADQPKDVKKTFDI 1380 	1381 LNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPFTL 1440 	1441 FRVVRLARIGRILRLVRAARGIRTLLFALAMSLPSLFNIGLLLFLVMFIYAIFGMSWFSK 1500 	1501 VKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQDSCQQPQIA 1560 	WWEKFDPEASOF		1681 DTWKTWMEEKFWEANPFKKLYEPIVTTKRKEEEGGAAVIQRAYRKHMEKAVKLRLKDRS 1740 	1741 SSSHOVFCNGDLSSLDVAKVKVHND 1765 	ULT 6 06597 AAY06597 standard; Protein; 1765 AA.

1765 AA;

Seguence

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New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
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/note= "domain IV transmembrane segment S1'
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/note= "domain IV transmembrane segment S6"
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/label= DIII-SS1
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N-PSDB; AAX87601.
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29-JAN-1998;
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Length 1765;
                    Indels
                   66;
 DB 20;
                  94; Mismatches
Score 8153;
Pred. No. 0;
88.98;
                    Matches 1569; Conservative
          Similarity
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5-224a-2.rag	Domain 159.179 //octe= "transmembrane domain DI-193.212 //octe= "transmembrane domain DI-19.240 //octe= "transmembrane domain DI-Domain 257.276	/not Domain 342. Jonain 356. Domain 770. Domain 569.	Domain 606629 Anote= "transmembrane domain DII-Domain 655684 Common 665684 Common 665684 Common 665684 Common 665684 Common 701720 Common 701720 Common 600601 Common 701720 Common 600601 Common 765760 Common 600601 Common 765760 Common 600601 Common 765760 Common 600601 Common 60060	omain omain omain omain omain omain	Domain 12641289 Jonean 12641289 Jonean 13431356 Jonee "transmembrane domain DIII 13431356 Jonee "transmembrane domain DIV-Domain 700tes "transmembrane domain DIV-Domain 14791469	FT
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(UYYA) UNIV YALE

SG; Waxman s, Dib-Hajj

2001-103147/11.

N-PSDB; AAF30103

השנבובונ מכום molecules encoding human tetrodotoxin resistant s channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -

Example 3; Fig 7B; 162pp; English

The present sequence is that of novel mouse tetrodotoxin resistant solium channel NaN, as deduced from the Scnlla gene (see AAF30103) isolated from a mouse trigemical ganglia cDNA. The sequence shows 68% similarity to human NaN (see AAB20121). NaN belongs to the a subunit voltage-gated sodium channels underlie the generation and propagation of impulses in sexcitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal curons. NaN polypeptides can be obtained by recombinant expression, and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate subject useful as diagnostic agents.

1765 AA; Sequence

LMIRISVHSVFSMFIICTVIINCMFMAN--SMERSFDNDIPEYVFIGIYILEAVIKILAR 178 GFIVDEFSFLRDPWNWLDFIVIGTAIATCFPGSQV-NLSALRTFRVFRALKAISVISGLK 237 KEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWE 357 VIVGALLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASNKDCFE 297 1 MEERYYPVIFPDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASR 60 RLYRQILRTSG1YFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEKMFQ Length 1765; 22; 66 DB Score 8153; E Pred. No. 0; 94; Mismatches 88.9%; Conservative Best Local Similarity Matches 1569; Conserv Query Match 121 179 181 238 241 298 301 358 361 121 421 Q Dp Dp q g ð δ ò g g q οy δ δ ΩŽ ά

1077 TEVPNRSQCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPD 1257 FEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMK 1317 FSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQDSCQQP 1557 999 717 777 900 657 837 897 957 597 FGTKFNKTAYATQERPRRRWHMDNFYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIV QSFCCKKCRRKNSPKPKFTTESFAGENKDS1LPDARPWKEYDTDMALYTGQAGAPLAPLA EVEDDVEYCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQS PTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSW DNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLS DNNRSFLASLRVERVERLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRL FVLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHAL 1FLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLMNLPSLKSFRTLRALRPLRALS **QFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDF** CFPCGKNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMD FDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFP 1078 1319 478 481 541 598 601 658 661 718 720 778 179 838 868 899 928 1138 1198 1199 1258 1259 1318 1378 1438 1438 1498 1498 Q qq . q οy ζ ·δ . 6 .g

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Sequence

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The present sequence is that of novel human tetrodotoxin resistant sodium channel NaN, as deduced from a CDNA clone (see AAP3010) isolated from human dorsal root ganglia tissue. NaN belongs to the a-subunit, voltage-gated sodium channel protein family. It produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal signalia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN polypeptides can be obtained by recombinant expression, to screen for compounds that modulate sodium channel.
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              SQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDS
                                                                             tqfiqysslsdfadalpeplrvakpnrfqflmmdlpmvmgdrlhcmdvlfafttrvlqns
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                                                      52;
                                       Length 1791;
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                                      73.1%; Score 6709; Dilarity 72.9%; Pred. No. 0; Conservative 179; Mismatches
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         ETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTVS
                               PKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSS
                                        GALIFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIV
                                                                         VFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQCNISNYSWKVPQVNFDNVGNAYL
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This protein comprises the human hHI voltage-regulated sodium channel protein that can be used in a novel system for enhancing cardiac dignal sensing by cardiac pacemakers through genetic treatment. A claimed system for delivering genetic material (GM) comprises a reservoir containing GM and a device for delivering it comprises a reservoir containing GM and a device for delivering it to myocardial cells (MC) at a specific location. The GM increases the amplitude of the cardiac signal, improving the signal-to-noise (S/N) ratio that is sensed by the electrode of a pacemaker. Also claimed are: (I) an implantable delivery system comprising a cardiac for delivering this through a catheter, the tip of MC and system for delivering this through a catheter, the tip of MC and system for delivering this through a catheter, the tip of MC and system for a pacing electrode on an inner wall of the heart, close to the site where the GM is delivered. The system is used atrial and ventricular MC and improves the sensing of cardiac signals by the pacemaker and the S/N ratio of atrial p-waves. The preferred GM comprises DNA (see AAV09029) or RNA encoding hHI.

for delivering genetic material to heart - comprises oir, catheter and optionally pacing electrode for delivering nnel protein, useful for, e.g. improving sensing by pacemaker

97WO-US05556. 96US-0682433

04-APR-1997; 17-JUL-1996;

22-JAN-1998

Homo sapiens WO9802040-A1

.rag

us-09-646-:224a

(MEDT) MEDTRONIC INC

Morissette J,

WPI; 1998-110247/10. N-PSDB; AAV09029.

Disclosure; Page 41-47; 73pp; English

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reservoir,

System

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Ifnmlimctiltncvfma-----qhdpppwtkyveytftaiytfeslvkilarafclh 184
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                                                                                                                                                                                                                                                                                                                                                                                                          | ||: :|||||||:| |||:|||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
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                                                                                                                                                                                  NFRPFTSDSLAAIKKRIAIQKER-----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGDI 69
                                                                                                                                                                                                                                EFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGAL
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Score 4712.5; DB 19; Length 2016
Pred. No. 0;
1; Mismatches 434; Indels 247;
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                                                                                           Conservative 281;
         51.4%;
50.2%;
                                                      Similarity
                                                                                           971;
Query Match
Best Local S
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                                                                                                                                                       channel; sodium channel; hH1; human; cardiac cell; heart;
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06-JUL-1998 AAW23994;

AAW23994
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2 5	458	FFMRGSKTAQASA 47	9 .
3 2	477	GCCCGCCTTLTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	, <u> </u>
ą	544	: shhtsllvpwplrrtsaqqqpspqtsapghalhgkknstvdcngvvsl 60	m
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6 6	686	75	7
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સ્ વ	856 1016	TTESFAGENKDSILPDARPWKEYDTDMALYTGQAGAPLAPLAEVEDDVEYCGEGG 91	0 65
7. q	911	LSIQ 95 LSIQ 95 	6 24
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<u>ک</u> ۾	1014	SFIIFVILLSSGALIFEDVNLPSRPOVEKLLRCTDN 10 	73
Ş q	1074	IFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLMNLFSLKSFRT 11:	26
ž g	1127	GVNLFSGKFGRCI 11 : gvnlfagkfgrci 13	86 64
3y 3b	1187 1365	12	42

New KVLQT1 and SCN5A genes, which contains alterations or mutations, useful in diagnostic/prognostic or drug screening methods, particularly in mutational analyses for screening individuals with or at risk for long QT syndrome. 1903 MMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSII 1422 1542 AKEHC-----NSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESE 1595 1656 MGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKRKEEEQ 1715 1243 MNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQD 1302 IFWTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMII 1362 LFLVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLE. SCN5A; Long QT syndrome; LQTS; cardiovascular disease; Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening; mutant; mutein. ¥ AAB82242 standard; Protein; 2015 09-AUG-2000; 2000WO-US21660. 09-AUG-1999; 99US-0147488. 17-MAR-2000; 2000US-0190057. (UTAH) UNIV UTAH RES FOUND Human SCN5A mutant delF1617 (first entry) Splawski I; 1716 GAAVIQRAYRKHM 1728 | |||||:|:|: 1904 samviqrafrrhl 1916 WPI; 2001-290564/30. WO200124681-A2 Homo sapiens 21-JUN-2001 Keating MT, 12-APR-2001 AAB82242; RESULT 10 AAB82242 1485 1363 1425 1303 1483 us-09-646-224a-2.rag

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-; 76pp; English

The present sequence is that of the claimed delF1617 mutant of the human SCN5A protein. The mutant is encoded by an SCN5A mutant gene carrying a deletion of the TTC codon for Phe-1617. Mutations of the SCN5A gene are implicated in Romano-Ward syndrome, the autosomal dominant form of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene lead to the following amino acid alterations in the encoded protein: D11144, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCNAA gene. Setul the present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing $\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\times}\overset{\mathrm{M}}{\overset{\mathrm{M}}{\overset{\mathrm{M}}}{\overset{\mathrm$

2015 AA; Sequence

30; AMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNV 405 604 lgagdpeatspgshllrpvmlehppdtttpseepggpgmltsgapcvdgfee---pgarg 660 PPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS 129 -----KTRKS-----FFMRGSKTAQASA 476 RALSAVSILTITIQEQEKFQEPCFPCGKNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTE 575 LAITICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHG 635 NFRPFTSDSLAAIKKRIAIQKER----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGDI 69 130 VFSMFIICTVIINCMFMANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD **EFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGAL** ::||||| ||||||:||||:||||||| | ||::: igsvkkladvmvltvfclsvfaliglqlfmgnlrhkcvrnftalngtngsveadglvwes ----SNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFL sgteecgedrlpksdsedgpramnhlsltrglsrtsmkprssrgsiftfrrrdlgseadf :| |: :: addenstareseshhtsllvpwplrrtsaggqpspgtsapghalhgkknstvdcngvvsl ----VDLFDEHVDPLHRQ LRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPA--------Length 2015; Indels AAETEAKEKMFQEAQOLLREEKEALVAMGIDRSSLNSLQASSFSP----SDSEDDASKN-----PQLLEQTKRLSQNLP------Score 4712; DB 22; Pred. No. 0;); Mismatches 430; Query Match 51.4%; So Best Local Similarity 50.2%; Pr Matches 972; Conservative 280; S----S 12 70 15 72 184 424 516 244 346 364 406 458 484 477 502 661 216 δ g δy 엄 δy 셤 δy Db Qy q QY QQ qq Q οy QQ δy QQ Óγ οy ογ ολ ŏ OD

1424 mnnlqlalariqrglrfvkrttwdfccgllrhrpqkpaalaaqgqlpsciatpysppppe 1015 ESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDL 1652 SPRKKSDAVSMLSECSTIDLN---DIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKR 1013 IFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMII 1362 tek------vpptrketgfeegegpggtpgdpepvcvpiavaesdtddgeedeen 1065 755 815 695 897 1066 slgteeesskqqesqpvsgwprgppdsrtwsqvsatasseaeasa-sqadwrqqwkaepq KSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDN 1363 MMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSII GLLLFLVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPM LE-AKEHC-----NSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATE WNVFDSIVALLSLADVLYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGA LGNLTVVLTIVVFIFSVVGMRLFGTKFNKTAYATQERPRRRWHMDNFYHSFLVVFRILCG TTESFAGENKDSILPDARPWKEYDTDMALYTGQAGAP --- LAPLAEVEDDV -- EYCGEGG 911 ALPTSQHSAGVQAGDL-----PPETK---QLTSPDDQGVEMEVFSEEDLH----LSIQ IFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLM------NLPSLKSFRT LRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCI NGTDINMYLDFTEVPNRSQCNISNYS----WKVPQVNFDNVGNAYLALLQVATYKGWLEI KTKVQLALDRFRRAFSFMLHALQSFCCKKCRRK----1303 1014 1016 1243 1545 721 989 781 969 156 868 856 957 1074 1127 1187 1425 1485 1423 1480 1540 1720 1593 Y de Y de ο_γ οŽ O CXqq ζ 9 3 62 CA do do do δ j.p 0y 0b 0y 9. 8. 9d 9. 9d QY 62

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                                                                                     AMPRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNV 405
                                                                                                                                                                                                                                                                                                                                  AAETEAKEKMFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSP-----KKRKFFG 457
                                                                                                                                                                                                                                                                                                                                                                                            -----FWRGSKTAQASA 476
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       || |:| | || 604 lgagdpeatspgshllrpvmlehppdtttpseepggpgmltsgapcvdgfee---pgard
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                                                                     VFSMFIICTVIINCMFMANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD
                                                                                                                                                                                          LRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPA-----------
                                                                                                                                                                                                                                                      ----SNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFL
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                                                                                                                                EFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGAL
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                                                       The present sequence is that of the protein encoded by the human SCN5A gene. This gene is implicated in Romano-Ward syndrome, the autosomal dominant form of Long OT syndrome (LOTS). Novel mutations have been identified in the gene using single strand conformation polymorphism analysis. These result in the following amino acid alterations: Dilatvi, LEGUY, delFi617, R1631L, EDT84K and S1787N. Isolated human polymorphides comprising such a mutation (see AAB82240-45) are claimed. Knowledge of the mutations provides means for assessing a risk in a human subject for LOTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene.
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                                       PMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKE
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                                                                                                                                                                                                          SCN5A; Long QT syndrome; LQTS; cardiovascular disease; Romano-Ward syndrome; diagnosis; prognosis; therapy;
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50.2%; Pred. No. 0;
ive 281; Mismatches
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N-PSDB; AAF30825
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17-MAR-2000;
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12-APR-2001

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2000WO-US21660. 99US-0147488. 2000US-0190057.

09-AUG-2000;

12-APR-2001

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(UTAH) UNIV UTAH RES

17-MAR-2000; 09-AUG-1999;

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1541
1303 IFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMII 1362
                                                                                                                                                                                         MMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSII 1422
                                                                                                                                                                                                                       1542 AKEHC ----- NSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESE 1595
                                                                                                                                                                                                                                                                                                                    DPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMV 1655
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                             1074 IFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLM------NLPSLKSFRT
                                                                                                                   NGTDINMYLDFTEVPNRSQCNISNYS----WKVPQVNFDNVGNAYLALLQVATYKGWLEI
                                                                                                                                                                                                                                                                            LFLVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCN5A; Long QT syndrome; LQTS; cardiovascular disease; Romano-Ward syndrome; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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28;

Gaps 69

Length 2016;

Score 4711.5; DB 22; Length 2016 Pred. No. 0; 9; Mismatches 433; Indels 255;

70 PPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS 129 | ||: :|||||||:| |||:|||| :||:||| ||::| ||:|| ::| |||| pqeligepledidpfystqktfivlnkgktifrfsatnalyvlspfhpvrraavkilvhs 131 130 VFSMFIICTVIINCMFMANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD 183

72

Oy Ob

qa

15 NFRPFTSDSLAAIKKRIAIQKER-----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGDI

Conservative 279; 51.4%; 50.1%; 1

Similarity

Query Match Best Local S Matches

970;

243

184

132 lfnmlimctiltncvfma-----qhdpppwtkyveytftaiytfeslvkilarafclh

184 EFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGAL

243 290 303 345 363

291

----SNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFL

244 LRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPA-------

423

AAETEAKEKMFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSP-----KKRKFFG 457

406

346 AMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNV

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The present sequence is that of the claimed D1114N mutant of the human SCN5A protein. The mutant is encoded by an SCN5A mutant of the gene in which a G/A mutation allers codon 1114 from GAC to AAC.

Mutations of the SCN5A gene are implicated in Romano-Ward syndrome, the autosomal dominant form of Long OT syndrome (LQTS). Mutations of the SCN5A gene lead to the following amino acid alterations in the encoded protein: D1114N, L1501V, delF1517, R1623L, E1784K and S1787N. Knowledge of the mutations provides can assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene.

Wote: The present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing (see AABB2220).
                                                                                                                                                                                                                                                                 New KVLQT1 and SCN5A genes, which contains alterations or mutations, useful in diagnostic/prognostic or drug screening methods, particularly in mutational analyses for screening individuals with or at risk for
                                                                                                                                                                                                                                                                                                                                                              Claim 31; Page -; 76pp; English.
                                                                                                                                                                                            Splawski I;
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g	424	iaeteekekrfqeamemlkkehealtirgvdtvsrsslemsplapvnsherrskrrkrms 483	
ογ	458	-FEMRGSKTAQASA 47	
qq	484	${\tt gteecgedrlpksdsedgpramnhlsltrglsrtsmkprssrgsiftfrrrdlgse}$	
ò	477	KNPQLLE	
QΩ	544	ddenstareseshhtsllvpwplrrtsaqgqps	
ογ	502	LFDEHVDPLHR	
qq	604	jfee	
ογ	516	RALSAVSILTITIQEQEKFQEPCFPCGKNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTE 575	
qq	199	lsavsvltsaleeleesrhkcppcwnrlagryliweccplwmsikggvklvvmdpft	
οy	576	LAITICIIINTVELAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHVFRHG 635	
οp	721	ivlntlfmalehynmtsefeemlqvgnlvftgiftaemtfkilaldpyyyfqq	
Oy Dp	636	WNVFDSIVALLSLADVLYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGA 695 [: : : :: :	
ò	969	VVGMRLFGTKFNKTAYATQERPRRRWHMDNFYHSFLVV	
Q	839	6	
٥y	756	NWWGCWQDMDGSPLCIIVFVLIWVIGKLVVLNLFIALLLNSFSNEEKDGSLEG	
qq	868	<pre>ewietmwdcm-evsgqslcllvfllvmvignlvvlnlflalllssfsadnltapde-dre 955</pre>	
δ	816	CCKKCRRKNSPKPK	
QQ	926		2
δý	856	TESFAGENKDSILPDARPWKEYDTDMALYTGQAGAPLAPLAEVEDDV	
qq	1016	tek	S
Οý	911	LPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEE	
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οy	955	TIDLNDIFRNLQKTVSPKKQPDRC	o.
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<u> </u>	1241	CIDNIETITELEERILNWYKERTRITSAWWHEDELYVVVVSUESLM - :: :	v C
ò	12	FCILGVNLFSGKF 11	
점	30	shrthalrphralsrfegmrvvvnalvgaipsimnvllvclifwlifsimgvnlfagkf 13	
ò	1183	RCINGTDINMYLDFTEVPNRSQCNISNYSWKVPQVNFDNVGNAYLALLOVATYKG	80
g	1361	:	
ογ	1239	LYFVVFIIFGSFFTLNLFIG	80
qq	1421		0
ογ	1299	GGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVL 135	æ
QQ	1481		0

New KVLQT1 and SCN5A genes, which contains alterations or mutations, useful in diagnostic/prognostic or drug screening methods, particularly in mutational analyses for screening individuals with or at risk for long QT syndrome LPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRK 1711 MLE-AKEHC-----NSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTAT 1591 NMIIMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVV SCNSA; Long QT syndrome; LQTS; cardiovascular disease; Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening; mutant; mutein. AAB82245 standard; Protein; 2016 AA. 09-AUG-2000; 2000WO-US21660. 1712 EEEQGAAVIORAYRKHM 1728 || | |||||:|:|: 1900 heevsamvigrafrrhl 1916 09-AUG-1999; 99US-0147488 17-MAR-2000; 2000US-0190057 (UTAH) UNIV UTAH RES FOUND (first entry) mutant S1787N. Splawski I; WPI; 2001-290564/30. W0200124681 A2. Homo sapiens. Keating MT, 21-JUN-2001 Human SCN5A 12-APR-2001 AAB82245; RESULT 13 1780 1652 1359 1539 1592 AAB82245 \$. 6 . 6 . 6 . 6 . 6

Claim 31; Page -; 76pp; English.

The present sequence is that of the claimed S1787N mutant of the human SCNSA protein. The mutant is encoded by an SCNSA mutant of the mutant in which a G/A mutation alters codon 1787 from AGT to AAT. Mutations of the SCNSA gene are implicated in Romano-Ward syndrome, the autosomal dominant form of Long QT syndrome (LQTS). Mutations

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newly discovered in the SCN5A gene lead to the following amino acid alterations in the encoded protein: D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LOTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene. Note: The present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing (see AAB82220).
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Ifumlimctiltncvfma-----qhdpppwtkyveytftaiytfeslvkilarafclh
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1302 tek-----vpptrketgfeegegpgggtpgdpepvcvpiavaesdtddgeedeen 1065 1304 1424 IFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMII 1362 MMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSII 1422 897 815 855 910 926 slgteeesskqqesqpvsgwprgppdsrtwsqvsatasseaeasa-sqadwrqqwkaepq SPRKKSDAVSMLSECSTIDLN---DIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKR EWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETR ---NSPKPKE TTESFAGENKDSILPDARPWKEYDTDMALYTGQAGAP---LAPLAEVEDDV--EYCGEGG KSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDN MNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQD STLVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLL LELVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLE-LGNLTVVLTIVVFIFSVVGMRLFGTKFNKTAYATQERPRRWHMDNFYHSFLVVFRILCG ALPTSQHSAGVQAGDL-----PPETK---QLTSPDDQGVEMEVFSEEDLH----LSIQ NGTDINMYLDFTEVPNRSQCNISNYS----WKVPQVNFDNVGNAYLALLQVATYKGWLEI DPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMV MGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKRKEEEQ KTKVQLALDRFRRAFSFMLHALQSFCCKKCRRK----911 1245 1425 1014 1305 1365 1243 1485 1363 1545 1423 1483 1542 816 1016 1066 957 1125 1185 1187 1303 1605 1724 1784 839 868 926 1596 1656 969 756 1127 g oy Oy ĊΣ Db QY Q δ рь . 2у ୍ୟ ବର୍ଷ ପ୍ରଥମ ବ୍ୟକ୍ତ ପ୍ରଥମ

GAAVIQRAYRKHM 1728

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Gene in which a C/G mutation alters coden 1501 from CTG to GTG.

Mutations of the SCN5A gene are implicated in Roomano-Ward syndrome, the autosomal dominant form of Long QT syndrome (LQTS). Mutations callerations in the encoded protein: D114M, L1501V, delF1617, R1621L, E1784K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene.

Note: The present sequence is not shown in the Sequence Listing derived from the KVLQT-1 sequence given in the Sequence Listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 NFRPFTSDSLAAIKKRIAIQKER----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGDI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or mutations,
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                                                                                                                                                                                                                            no-Ward syndrome; diagnosis; prognosis; therapy; screening; mutant; mutein.
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2000US-0190057.
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                          EFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGAL
                                                             LRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPA-------
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                    IFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLM-----NLPSLKSFRT
                              LRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCI
                                                                       NGTDINMYLDFTEVPNRSQCNISNYS----WKVPQVNFDNVGNAYLALLQVATYKGWLEI
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Romano-Ward syndrome; diagnosis; prognosis; therapy;
drug screening; mutant; mutein.
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which contains alterations
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                                                                                                            New KVLQT1 and SCN5A genes,
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                                     RES
                                                             Splawski
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                                     UTAH
           17-MAR-2000;
                                     (UTAH ) UNIV
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eful in diagnostic/prognostic or drug screening methods, particularly mutational analyses for screening individuals with or at risk for or mutations, Claim 31; Page -; 76pp; English. QT syndrome long

The present sequence is that of the claimed E1784K mutant of the human SCN5A protein. The mutant is encoded by an SCN5A mutant gene in which a G/A mutation alters codon 1784 from GAG to AAG. Mutations of the SCN5A gene are implicated in Romano-Ward syndrome, the autosomal dominant form of Long OT syndrome (LOTS). Mutations newly discovered in the SCN5A gene lead to the following amino acid alterations in the encoded protein: D1114N, L1501V, delP1617, CR1621L, E1784K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for drugs useful in treating a human having a mutation in the SCN5A gene. CR pote: The present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing (see AAB82220).

Gaps Length 2016; 247; Indels DB 22; Query Match 51.3%; Score 4708.5; DB 22; Best Local Similarity 50.2%; Pred. No. 0; Matches 970; Conservative 280; Mismatches 436;

2016 AA;

Sequence

29;

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345 ----SNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFL 291

406 AAETEAKEKMFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSP-----KKRKFFG

-----FFMRGSKTAQASA 476 sgteecgedrlpksdsedgpramnhlsltrglsrtsmkprssrgsiftfrrrdlgseadf 543 S----S 458 484

à	477	DSEDDASKNPQLLEQTKRLSONLP	
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ργ	. 96	VLTIVVEIFSVVGMRLFGTKFNKTAYATQERPRRRWHMDNFYHSFLVVFRILCG 75	
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

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645.826 Million cell updates/sec February 26, 2002, 22:39:50 Run on:

US-09-646-224A-2 9173 1 MEERYYPVIFPDERNFRPFT......VFCNGDLSSLDVAKVKVHND 1765 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

212252 seqs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMARIES

SUMMARIES	Description	43-41	325-16 Sequence 16,	25-10 Sequence 10,	Sequence 12,	-417-2 Sequence 2, A	Sequence 7,	-020B-3 Sequence 3,	320B-4 Sequence 4,	11 Sequence 11,)20B-9 Sequence 9,	325-15 Sequence 15,	793-3 Sequence 3, 1	3 Sequence 3,	Sequence 4,	4 Sequence 4,	7	19 Sequence 19,	-8 Sequence 8,	325-2 Sequence 2,	325-8 Sequence 8	Д	35-675B-4 Sequence 4, Appl:	-543A-51 Sequence 51,	305C-51 Sequence 51,	-257A-7 Sequence 7, P	45-206A-2 Sequence 2,	
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28	BESULT 1 SEGUENCE 10, APPLICATION 15,08843417 SEQUENCE 10, APPLICATION 15,08843417 PATELICANT: Herman, Ronald C APPLICANT: Delgado, Stephen G APPLICANT: Belgado, Stephen G APPLICANT: Balgado, Stephen G CONFESPONDENCE ADDRESS: ADDRESSEE: Heller Ehrman White & McAull STREET: 525 University Ave CITY: Palo Alto STREET: 525 University Ave COMPUTER: IBM PC compatible COMPUTER: Balgado Als COMPUTER: April 15, 1997 CLASSIFICATION NUMBER: 28340-P1 TELECOMMUNICATION NUMBER: 28340-P1 TELECOMMUNICATION INFORMATION: TELEPHONE: (415)-324-0638 INPORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 1956 amino acids TYPE: amino acid STRANDEDNESS: unknown MOLECULE TYPE: Peptide ANTI-SENSE: NO SEQUENCE CHARACTERICAL: NO ANTI-SENSE: NO	Query Match Best Local Similarity
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λς Q	122	MIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILAR 178 :: : : : AIKVSVHSWFSLFIIVTILVNCVCMTRTDLPBKIEYVFTVIYTFEALIKILAR 175	
oy Dp	179 176	GFIVDEFSFLRDPWMWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISG 235	
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λς Q	554	61 70	
AC qa	614	IFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDNNRSFLASLRVLRVF 673 	
. qo	674 765	KLAKSMPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNKTAYATQE 731 	
λς Q	732	RPRRRWHMDNEYHSELVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLN 791 : : : : : : : :	
λς qo	792	LFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCCKKCR 846	
γς qo	937	RKNSPKPTTESFAGENKDSILPDARPWKEYDTDMALYTGQ 888	
oy.	889 995	VEYCGEGGALPTSQHSAGV 9	

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APPLICANT: Mandel, Gail
APPLICANT: Halegous, Simon
APPLICANT: Halegous, Simon
APPLICANT: Halegous, Simon
APPLICANT: Halegous, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Usi.
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                                                      AWCWLDFLIVVVSVLSL-----MNLPSLKSFRTLRALRPLRALSQFEGMKVVVYALIS
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RWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPNLPNSNGTRGDC
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                                                                                                                                                                                                                                                                              YAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTK
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QAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLND---
                                             IFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFES
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Patent No. 6110672
GENERAL INFORMATION:
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US-08-836-325-16
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                          QMLDRLKKEQEEAEAIAAAAAEYTSIRRSRIMGLSESSSETSKLSSKSAKERRNRRKKN
                                                                       QKKLSSGEEKGDAEKLSKSESEDSIRRKSFHLGVEGHRRAHEKRLSTPNOSPLSIRGSLF
                                                                                                                                                        TKRLSQNLPVD-----LF
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  EAQQLLR - - - EEKEALVA -
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 GOLDSTEIN & FOX P.L.L.C
N. W., Suite 600
                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 961; Conservative 281; Mismatches
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ER: 0917.0240002
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
KESSLER,
 : STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               1969 amino acids
                                                                                                                                                                                                                                                                                                                           NAME: Ludwig, Steven R
REGISTRATION NUMBER: 3(
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                        202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-325-16
                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                            20005-3934
                                                   COUNTRY:
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                                                                                                                                                                                         Length 1984;
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                                                                                                                                                                                       Ouery Match 49.5%; Score 4541.5; Best Local Similarity 48.9%; Pred. No. 0; Matches 954; Conservative 291; Mismatches
            0917.0240002
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 REGISTRATION NUMBER: 36,203
              REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2640
TELEPRAX: 202-371-2540
                                                                INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                            LENGTH: 1984 amino acids
                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-10
                                                                                                          amino acid
                                                   TELEFAX:
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APPLICANT: Halegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden. Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                     1617
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                                                                                                                                                                                                                                                      LARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSWFSKVKKGS
                                                                                                          SVGIFYFVSYIIISFLVVVNMYIAVILENFSVATEESTEPLSEDDFEMFYEVWEKFDPDA
                                       VVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFRVVR
                                                                                                                                                GIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKE-----HCNSSSODSCOOP
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N. W., Suite 600
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILIND DATE: 02 NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILIND DATE: 07-70U-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILIND DATE: 02 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08836325 Patent No. 6110672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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1890 VKNISS 1895
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Oy Dp	668 837	RVLRVEKLAKSMPTLNTLIKIIGHSVGALGNLTVVLTIVVEIFSVVGMRLFGTKFNK-TA :	726 896
Oy Dp	727	YATQERPRRWHMDNEYHSELVVFRILCGEWIENWWGCWQDMDGSPLCIIVFVLIMVIGK	786 955
oy Pp	787 956	LVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALGSFCCKKCR	846 1014
Oy Dp	847	<u>a</u> – <u>a</u>	904
oy D	905	QG-VEM	956
Qy	957	P-RKKSDAVSMLSECSTIDLNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDK 	01
Oy Dp	1014	YQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLL : : :::::::::::::::::::::::	7 2
Oy Dp	1074	IFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLMNLPSLKSFRT : : : : : :	1126
Qy Dp	1127	LRALRPLRALSOFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCI 	1186
Qy Dp	1187 1350	NGTDINWYLDFTEVPNRSQCNIS-NYSWKVPQVNFDNVGNAYLALLQVATYKGWLE	1241
Oy Dp	1242	IMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGG 	1301
oy op	1302	DIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMI 	1361
Qy Dp	1362 1529	IMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSI	1421
oy Dp	1422	IST-LVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIG	1480
oy op	1481	LLLFLVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPML 	1540
Qy Dp	1541	EAKEHCNSSSQDSCQOPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATE:	1592 1766
Oy Dp	1593 1767	ESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVWDL :	1652 1826
Oy Dp	1653 1827	PMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKE 	1712 1886

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APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Usi
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
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1713 EEQGAAVIQRAYRK-----HMEKMVKLRLKD 1738
                           1887 EEVSATIIQRAYRRYRLRQHVKNISSIYIKD 1917
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PRIOR APPLICATION DATA:
APPLICATION UNBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION UNBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION UNBER: 08/334,029
FILING DATE: 07-JUN-1995
PRIOR APPLICATION UNBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PatentIn Policy
                                                                                                                                       US-08-836-325-12
Sequence 12, Application US/08836325
Patent No. 6110672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER,
STREET: 1100 New York Ave.,
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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TOPOLOGY: not relevant
WALECULE TYPE: protein
(is-08-836-325-12)
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TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC
STATE: DC
COUNTRY: USA
ZIP: 20005-3344
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Oy Dp	130 VFSMFIICTVIINCMFMANSMERSFDNDIPEVVFIGIYILEAVIKILARGFIVDEFSFLR 189 11 1:1 1:1		q _Q	: : :
QY	190 DPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKK 		òy đầ	1073 NIFTFIFLLEMILKWVAFGFRRYFTSAMCWLDFLIVVVSV : : : : :
, oy	250 LVDVMVLTLECLSIFALVGQQLFMG1LNQKCIKHNCGPNPASNKDCFEKEKD		Q q	1126 TLRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVCLI
QY	302SEDFINGGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWE 		Qy Qu	1186 INGTDINMYLDFTEVPNRSQCNIS-NYSWKVPQVNF
Qy	358 RLYROILRTSGIYFVPFFVVVIFLGSFYLLNLTLAVVTMAYEEONRNVAAETERKEKMFO		Ç.	1241 EIMNAAVDSREKDEQPDFEANLYAYLYFVYFIIFGSFFTI
QY	418 BAQQLLRBEKEALVA		Qy Dp	1301 QDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVF
0y	454	· · ·	oy da	1361 IIMMAESADQPKDVKYTFDILNIAFVVIFTIECLIKVFAI 1
3 6	454		Δλ Dp	1421 IIST-LVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAP : : : 1590 IVGMFLAEMIEKYFVSPTLFRVIRLARIGRILRLIKGA
8 8 8	545 SARRSSRISLFSFKGRGRDLGSETEFADDEHSIFGDNESRRGSLFVPHRPRERRSSNISQ 474 ASASDSEDDASKNPQL	•	G G	1480 GLLLFLVMFIXAIFGMSWFSKVKKGSGIDDIFNFETFTGS
7	490		Qy da	1540 LEAKEHCNSSSQDSCQQPQIAVVYEVSYIIIS
oy g	548 KYLVWDCSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFEAUEHINDDNLKTILKIG 548 KYLVWDCSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIG 5720 FFIXMCSPVWTKFKTIVFTVPTVMDPPVDLAITICIVINTI-RAAMEHHUMTEREVINTAVO	· · · · ·	. άα :	1592 EESEDPLGEDDFEIFYEVWEKFDPEASGFIQYSALSDFAL :
Qy Db	608 NWVFTGIFIAEMCLKIIALDPYHYFHGWNVFDSIVALLSLADVLYNTLSD-NNRSFLAS		QY QD	1652 LPWVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKE
Qy Db	667 LRVLRVFKLAKSWPTLNTLIKLIGHSVGALGNLTVVLTIVVFFFSVVGMRLFGTKFNK-T :		G C	1712 EEEGGAAVIQRAYRKHMEKMVKLRLKD 1738 :
Qy	726 AYATQERPRRRWHMDNFYHSFLVVFRILCGEWIENNWGCMQDMDGSPLCIIVFULIMVIG 785 : ::		RES US-	RESULT 5 US-08-843-417-2 : Sequence 2, Application US/08843417
Qy	786 KLVVLNLFIALLLNSFSNEEKDGSLEGETRYTKVQLALDRFRRAFSFMLHALGSFCCKKC 845		Δ.	; Patent No. 6184149; GENERAL INPORMATION: APPLICANT: Herman, Ronald C APPLICANT: Delgado, Stephen G
Qy	846	<u>- 1012 1</u>	.e	APPLICANT: Fish, Linda M APPLICANT: Sangameswaran, Lakshmi APPLICANT: Rabert, Douglas K TITLE OF INVENTION: CLONED PERIPHERAL NERVE
Qy Db	904 EYCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQG-VEMEVFSEEDLHLSI 955 1051 I.		IN IN IN	TITLE OF INVENTION: TETRODOTOXIN-RESISTANT S NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Heller Ehrman White & McAuliffe
oy ob	956 QSP-RKKSDAVSMLSECSTIDLNDIFRNLQKTVSFKKQPDRCFPKGLSCHFLCHKTDK		**************************************	STREET: 525 University Ave CITY: Palo Alto STATE: CA COUNTRY: U.S.A. COUNTRY: U.S.A. CIP: 94301
Ķ		-	••	COMPUTER READABLE FORM:

'E SODIUM CHANNEL alpha-SUBUNIT NFDNVGNAYLALLQVATYKGWL 1240 ||||||| || ||:|||||:|||| NFDNVGLGYLSLLQVATFKGWM 1409 TINLFIGVIIDNFNQQKKLGG 1300 |||||||||||||||||||||||||||| TINLFIGVIIDNFNQQKKKLGG 1469 | |||: : :::| | LAFEDIXIEKKKTIKIILEYAD 1230 |:::|: SLVTLVANTLGYSDLGPIKSLR 1290 VFDLVTSQVFDVIILGLIVLNM 1360 :|||||;||||;||||||| IFDLVTNQAFDITIMVLICLNM 1529 SVLSLM-----NLPSLKSFR 1125 ALROHYFTNGWNLFDCVVVVLS 1420 SLRHYYFTVGWNILYFVVVILS 1589 fe

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LSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPS 1060
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                                                                                                                                                                                                                                                       TAPEDDGEV-----WNLQLALARIQVLGHRASRAIASYISSHCRFR---WPKVETQLGM 948
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                                                         NLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVF
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              IGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKF - - NKTAYATQERPRRRHHMDNFYHSF
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                                             MTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDP
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FSIFITITILVNCVCMTRT-----DLPEKVEYVFTVIYTFEALIKILARGFCLNEFTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFRPFTSDSLAAIKKRIAIQKERKKSKDKAAAE----PQPRPQLDLKASRKLPKLYGDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSMFIICTVIINCMFMANSMERSFDNDIP---EYVFIGIYILEAVIKILARGFIVDEFSF
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                                                                                                                                                                                                                                                                                                                                                            Mismatches 443;
                                                                                                                                                                                                                                                                                                                                      DB 4;
                    Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                     49.1%; Score 4506; 50.7%; Pred. No. 0;
                                                                          ATTORNEY AGENT INFORMATION:
NAME: Schmonsees, William
REGISTATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEPHONE: (415)-324-0638
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                         APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                              dorsal root ganglia
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            962; Conservative 269;
                                                                                                                                                                                                                                                                                        ; CELL TYPE: peripheral nerve
US-08-843-417-2
                                                                                                                                                                                   1956 amino acids
                                                                                                                                                                                                                     not relevant
                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                         HYPOTHETICAL: Y ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            TISSUE TYPE:
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QY 1520 MLCLFQITTSAGWDTLLNPMLE-AKBHCNSSSQDSCQQPQIAVVYFVSYIIISF 1572	48.88;
Db 1652 MLCLFQITTSAGWDGLLSPILNTGPPYCDPNLPNSNGSRGNCGSPAVGIIFFTTYIILSF 1711	Best Local Similarity 48.1%; Pred. No. 0; Matches 950; Conservative 276; Mismatches 450; Indels
OY 1573 LIVVNMYIAVILENPNTATEESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADA 1632 	OY 11 PDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASRKLPK 64
OY 1633 LPEDLRVARPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFM 1692 Dh 1772 LSCPLBTBKDNONTLIOMFLELVEDREHGINT BEFRANT GESCEF DSC PRIMERED 1021	
1772 BOSE ENTERNEMONTELIGNOMENVESDATACEDILERELANNY ESESSEEDDENINMEENEM	0
QY 1693 EANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHM 1728 	<pre>Qy 125 ISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPPEYVFIGIYILEAVIKIIARGFIVDE 184 ,</pre>
RESULT 6	185 FSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALL
; Squence 7, Application US/08836325	184 FIFLKNEWNWEDFIVIIFALVIEFV-NDSNVSALKIFKVLKALKIISVIPGLKIIVGALI
; Patent No. 01106/2/ ; GENERAL INFORMATION: ; APPLICANT: Mandel, Gail	OY 245 RSYKKLYDDWAVLTEFCLSIFALVGQLFMGTLNOKGIKHNGGPNPASN 292
; APPLICANT: Halegoua, Simon ; APPLICANT: Borden, Laurence A. ; TITE OF INTERMITON, Docingery	293KDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTT
; IIILD OF INVENTION: FELLQUETA NETVOUS SYSTEM SPECIFIC; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization, TITLE OF INVENTION: X-ray Diffraction. Computer Molecular Modeling. Rational	Db 298 NSLDWNGTAFNRTVNMFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAG 357
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using ; TITLE OF INVENTION: Thereof; NUMBER OF SEQUENCES: 19	OY 328 LNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLL 387 [D] 358 RNPWGYFSPTFSWAFISIFRIAMODEWERLYROITHRAAGKTYWTFPVLVIFLGSFYLT 417
CORRESPONDENCE ADDRESS: ADDRESSER: STERNE KESSIER GOIDSTEIN & FOX P. 1. C	230 NI WT NIVYWAN V DDONONINA NEWDAY EVENEDOD - A COTT DEDVENTANTE.
STREET: 1100 New York Ave., N. W., Suite 600	43 418 NLILAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAASAESRDFSGA 47
ΞĘ	Qy 434 -GIDRSSLNSLQASSFSPKKRKFFGSKTRK
COMPUTER READABLE FORM: MEDITIM TYPE: Flower disk	DD 478 GGIGVFSESSSVASKLSSKSEKELKNRRKKKKQKEQAGEEKEDAVRKSASEDSIRKKGF 537
COMPUTER: FIDE OF COMPATIBLE COMPATIBLE SCHOOL SYSTEM: PC-DOS/MS-DOS	Cy 463 SFFWRGSKTAQ
; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	Db 538 QFSLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFNFKGRVKDIGSENDFADDE 597
; APPLICATION NUMBER: US/08/836,325 ; FILING DATE: 2-MAY-1997	483
; CLASSIFICATION: 514 ; PRIOR APPLICATION DATA:	Db 598 HSTFEDNDSRRDSLEVPHRHGERRPSNVSQASRASRGIPTLPMNGKMHSAVDCNGVVSLV 657
; APPLICATION NUMBER: PCT/US95/14251 ; FILIM DATE: 02-NOV-1995	503
; APPLICATION DATA: ; APPLICATION NUMBER: 08/482,401	658 GGPSALTSPVGQLLPEGTTTETEIRKRRSSSYHVSMDLLEDP-SRQRAMSMASILTNTME 71
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; FILING DATE: 02-100-1994	/ I/ DIBEBORÇINCEFCWINE ANNICET WOLCE FWENNING WITH SOME WITH TO LIVE AND LESS TO LIVE AND LESS TO LIVE AND LESS TO LIVE AND LIVE AND LESS TO LIVE AND LIVE AND LESS TO LIVE AND LIVE AND LESS TO LIVE AND LIVE AND LESS TO LIVE AND
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OCKET NUMBE ATION INFORM	650 DV-LYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVILIVVP
; TELEPHONE: 202-371-2600 ; TELEPAX: 202-371-2540	837 ELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVF
SEQUENCE CHARACTERISTICS:	Qy 709 IFSVVGMRLFGTKFNKTAYATQERPRRRWHMDNFYHSFLVVFRILCGEWIENMWGCM 765
TIVE: amino acids	Db 894 IFAVVGMQLFGKSYKECVCKISNDCELPRWHMHHFFHSFLIVFRVLCGEWIETMWDCM 951
	Oy 766 QDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDR 825
y wordcore like: peptide US-08-836-325-7	DD 952 -EVAGQIMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNL-AATDDDNEMNNLQIAVGR 1009
	QY 826 FRRAFSFMLHALQSFCCKKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTD 881
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LIVVVSVLSL------MNLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPAILN 1158
                                                                                                                                                                                                         VLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQCNI---SNYS--W 1213
                                                                                                                                                                                                                                               KVPQVNFDNVGNAÝLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFII 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP-----DDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTV
                                                                               SPKK--QPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVIL
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RESULT 7
US-09-024-020B-3
Sequence 3, Application US/09024020B
Sequence 10. 6030810
GENERAL INFORMATION:
APPLICANT: DELCADO, STEPHEN G.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
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351 367 411

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TETRODOTOXIN-SENSITIVE IL I-SUBUNIT AND A SPLICE VARIANT THEREOF #1.30 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: A2-250 R0020B-REG US/09/024,020B PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799 ΜS SODIUM CHANNEL OPERATING SYSTEM: PC-DOS/MS-DOS LAKSHMI CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE,
CITY: PALO ALTO : Floppy disk
IBM PC compatible TELECOMMUNICATION INFORMATION TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-322
INFORMATION FOR. SEQ ID NO. 3: SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US/09 FILING DATE: 16-FEB-1998 LENGTH: 1978 amino acids SANGAMESWARAN, REFERENCE/DOCKET NUMBER: STRANDEDNESS: single COMPUTER READABLE FORM: MEDIUM TYPE: Floppy MOLECULE TYPE: peptide NUMBER OF SEQUENCES: TITLE OF INVENTION: TITLE OF INVENTION: amino acid linear RY: U.S.A. 94304-1397 CLASSIFICATION: TOPOLOGY: COMPUTER: US-09-024-020B-3 COUNTRY: STATE:

125 185 245 SNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRV 350 Gaps 65 68 PDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKAA----AEPQPRPQLDLKASRKLPKL YGDIPPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRİ SFLRDPWNWLDFIVIGTA1ATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLR SVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGFIVDEF Length 1978; 271; Indels SVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPA----DB 3; 468; Query Match
47.9%; Score 4394.5;
Best Local Similarity 47.2%; Pred. No. 0;
Matches 925; Conservative 294; Mismatches 69 188 6 11 99 126 186 246 247 291 307

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| δb | | | Db 1470 KKI |
| Oy | | | Oy 1356 IV |
| qa | :
487 SAKERRNRRKRRQKELSEGEEKGDP | :
SAKERRNRRKKRKQKELSEGEEKGDPEKVFKSESEDGMRRKAFRLPDNRIGRKFSIMNQS 546 | |
| Qy | 467RGSK | RGSKTAQASASDSEDD | 1416 |
| QQ |
 S47 LLSIPGSPFLSRHNSKSSIFSFRGPG | : : | 1590 |
| QY | 483ASKNPQLLEQ | -ASKNPQLLEQTKR-LSQNLPVDL504 | OY 1475 SEI
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| qq | 607 ARERRSSYSGYSQCSRSSRIFPS | 607 ARERRSSYSGYSGYSGCSRSSRIFPSLRRSVKRNSTVDCNGVVSLIGPGSHIGRLLPEAT 666 | 15.35 |
| ې و | 505 | FDEHVDPLHRQRALSAVSILTIT-IQEQEKFQEPCFPCGKNLAS 547 FDEHVDPLHRQRALSAVSILTIT-IQEQEKFQEPCFPCGKNLAS 547 | 1708 |
| 3 8 | 548 KYLVWDCSDOWICTKKULRUTMPDF | | Qy 1588 NT |
| G G | 727 TFLIWECHPYWIKLKEIVNLIVMDPF | | 1768 |
| δο d | | | OY 1648 LVI
DD 1828 IAI |
| a à | /8/ NEVETGLETAEMELKLIAMDPIYIFQ | NLVFTGIFTAEMFLAKLIAMDPYYYFGEGWNIFDGFTVSLSEMELSLADVEGLSVLKS 843 | QY 1708 TK |
| g
G | 844 FRLLRVFKLAKSWPTLNMLIKIIGNS | 844 FRLERVFKLAKSWPTLNMIKKIIGNSVGALGULIVALIVAFIFAVVGMQLFGRRNN 1 723 | DD 1888 LR |
| ογ | 726 AYATQERPRRRWHMDNFYHSFLVVFR | AYATQERPRRWHMDNFYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIG 785 | PESULT 8 |
| qq | 904 CKINQECKLPRWHMNDFFHSFLIVFR | :: | S-09-024-020
Sequence 4 |
| Qy | 786 KLVVLNLFTALLLNSFSNEEKDGSLEGET | KLVVLNLFIALLINSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSF 840
 | GENERAL II SPELICAL APPLICAL |
| ΟŸ | 841 CCKKCRRKNSPKPKETTESFAGENKD | -DARPWKEYDTDMALYTGQAGAPLAP | |
| qq | 1017 MQAHFKQREADEVKPLDELYEKKA | MQAHFKQREADEVYPLDELYEKKANCIANHTGVDIHRNGDFQKNGNGTTSGIGSSVEK 1074. | TITLE O |
| Qy | 896 LAEVEDDVEYCGEGGALPTSQHSAGV | LAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSI 955 | NUMBER (|
| QQ | 1075 YIIDEDHMSFINNPNLTVRVPIAVGESDFENLNTED- | AVGESDFENLNTEDVSSESDP 1117 | ADDRE |
| Qy
Dp | 956 QSPRKKSDAVSMLSECSTIDLNDIFR
: :
1118 EGSKDKLDDTSS-SEGSTIDIRPEVE | QSPRKKSDAVSMLSECSTIDLNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHK 1009 : : | STATE |
| QY | 1010 TDKRKSPWVLWWNIRKTCYQIVKHSW | TDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLR 1069 | ZIP:
COMPUTED |
| QQ | 1172 VNIEEGLGKSWWILRKTCFLIVEHNW | FETFIFMILLSSGALAFEDIYIEQRKTIRTILE 1231 | COMPU |
| δλ | | NLPSLK | SOFTW |
| qq | | FTNAWCWLDFLIVAVSLVSLIANALGYSELGAIK 1291 | ; APPLIC |
| Oy
Dp | 1123 SFRTLRALRPLRALSQFEGMKVVVYA
 | SFRTLRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVVCLIFWLVFCILGVNLFSGKF 1182
 | CLASS: PRIOR AI APPLIC |
| Qy | 1183 GRCINGT-DINMYLDFTEVPNRSQC | NISNYSWKVPQVNFDNVGNAYLALLQVAT 1235 | FILING |
| qa | 1352 HYCFNETSEIRFEIDI VNNKTDCE | HYCENETSEIRFEIDI VNNKTDCEKLMEGNSTEIRWKNVKINFDNVGAGYLALLQVAT 1409 | REGIST |
| Qy
Dp | 1236 YKGWLEIMNAAVDSREKDEQPDFEAN
 | YKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQ 1295
 :: : : : : : | TELEP |
| Qy | 1296 KKLGGQDIFMTEEOKKYYNAMKKLGT
 | KKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGL 1355
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TINFORMATION:
CANT: DELGADO, STEPHEN G.
CANT: DELGADO, STEPHEN G.
CANT: DELGADO, STEPHEN G.
CANT: DELGADO, STEPHEN G.
CANT: FISH, LINNA M.
CANT: FISH, LINNA RONALD C.
CANT: SANGAMESKARAN, LAKSHMI
OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
OF INVENTION: SOBJUM CHANNEL I-SUBGNIT AND A SPLICE VARIANT THEREOF
R OF SEQUENCES: 43
SPONDENCE ADDRESS:
RESSEE: JANET PAULINE CLARK
RESSEE: JANET PAULINE CLARK
RESSEE: 3401 HILLVIEW AVENUE, MS A2-250
                                         /LINMIIMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCV 1415
                                                                     JENIGLLLELVWRIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDT 1534
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                                                                                                                                 VVLSIIST-LVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLP 1474
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TAPPLICATION DATA: US/09/024,020B
IGATION NUMBER: US/09/024,020B
NG DATE: 16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRKEEEQGAAVIQRAYRKHM-----EKMVKLRLKD 1738
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RRKQEEVSAVVLQRAYRGHLARRGFICRKMASNKLEN 1925
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PLICATION NUMBER: US 60/039,447
LING ADATE: 26-FEB 1997
LING ADATE: 26-FEB 1997
ME: CLARK, JANET P.
GIESTRATION NUMBER: 34,799
FERENCE/DOCKET NUMBER: R0020B-REG
FERENCE/DOCKET NUMBER: R0020B-REG
LEFPAN: (650) 852-3097
LLEFAX: (650) 852-302
ATION FOR SEQ ID NO: 4:
INGTH: 1988 amino acids
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UM TYPE: Floppy disk
UTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
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4, Application US/09024020B
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; TYPE: amino acid
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US-09-024-020B-4
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RESULT 9 US-08-836-325-11 ·デス

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QKKXSSGEEKGDXEKLSKSXSEXSIRXKSFHLGVEGHXRXXEKRLSTPNQSPLSIRGSLF
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127 LFSMLIMCTILTNCIFMTXXNPPXWTKNV-XYTFTGIYTFESLXKILARGFCVGEFTFLR
                                                                                                                                                                                STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494;
                                                                                                                                                                                            1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 47.8%; Score 4388.5; Best Local Similarity 48.0%; Pred. No. 0; Matches 934; Conservative 269; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0917.0240002
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/836,325 FILING DATE: 2-MAY-1997
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 07-JUN-1995
Application US/08836325
                                                                    Borden, Laurence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 09 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
                                        : Mandel, Gail
: Halegoua, Simon
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                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: (
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                                                                             TITLE OF INVENTION: P
TITLE OF INVENTION: S
TITLE OF INVENTION: X
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
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                            GENERAL INFORMATION:
                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3934
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              Patent No. 6110672
                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                      APPLICANT
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us-09-646-224a-2.rai

| CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 60/039,447 FILING DATE: 26-FEB-1997 ATTORNEY/ACENT INFORMATION: NAME: CLARK, JANET P. REGISTRATION NUMBER: 34,799 REFERENCE/DOCKET NUMBER: R0020B-REG TELECOMMUNICATION IUPRORMATION: TELEPHONE: (650) 852-3097 TELEPHONE: (650) 852-3097 TELEPHONE: (650) 852-3097 TELEPHONE: (650) 852-3097 TELEPHONE: (650) 858-5322 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 1976 amino acids TYPE: amino acids TYPE: anino acid STRANDEDNESS: single TOPOLGY: linear MOLECULE TYPE: peptide | OUETY Match Watch Best Local Similarity Watchs Best Local Similarity Watches 915; Conservative 293; Mismatches 478; Indels 269; Gaps Matches 915; Conservative 293; Mismatches 478; Indels 269; Gaps Matches 915; Conservative 293; Mismatches 478; Indels 269; Gaps Matches 11; PDERNFRPFTSDSLAAIKKRIOKERKSKOKAAAEPOPRPOLDLKASRKLPKL 65 | OY 291 SNKDCFEKEKDSEDFINGGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRY 350 11 |
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| Qy 1134. RALSOPEGMKVVVAALISAIPAILANVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINM 1193 P 1299. RALSOPEGMKVVVVAALISAIPAILANVLLVCLIFWLFSLIGVILFAGKFYECXNTTDGSR 1358 Qy 1194. YLDFTEVENRSQCNIS-NYSMKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAND 1248 S 1194. YLDFTEVPRRSQCNIS-NYSMKVPQVNFDNVGLGYLALLQVATYKGWLEIMNAND 1248 S 1194. YLDFTEVPRRSQCNIS-NYSMKVPQVNFDNVGLGYLALLQVATYKGWLEIMNAND 1248 S 1118.11.11.11.11.11.11.11.11.11.11.11.11 | OY 1428 RLEDSDISFPPTLERVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLENIGLLLFLVM 1487 1598 XIEXYEVS-PTLFRVIRLARIGRILRLXKGAKGIRTLLFALMMSLPALFUIGLLFLVM 1655 OY 1488 FIYALFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEA 1542 Db 1656 FIYALFGMSNFAYVKEXGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEA 1542 OY 1543KEHCNSSGOGOQDAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDDLG 1599 Db 1716 DPKKVHPGSSVEGOCQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDDLG 1599 Db 1716 DPKKVHPGSSVEGOCQNPSVGIFYFVSYIIISFLIVVNMYIAVILENFSVATEESTEPLS 1775 OY 1600 EDDFEIFYEVWEKFDPEASOFIOYSALSDFADALPEPLRAKPNKFOFLVMDLPMVWGDR 1659 1111111111111111111111111111111111 | RESULT 10 US-09-024-020B-9 SGQUENCE 9, Application US/09024020B SQUENCE 9, Application US/09024020B SQUENCE 9, Application US/09024020B SQUENCE 10 0030810 GENERAL INFORMATION: APPLICANT: BISH, LINDA M. APPLICANT: SANGAMESWARAN, LAKSHMI TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF CORRESPONDENCE ADDRESS: ADDRESSEE: JANET PAULINE CLARK STREET: 3401 HILLVIEW AVENUE, MS A2-250 CITY: PALO ALTO STREET: 0. A. COMPUTER: US.A. I IBM PC COMPATION: SOFTWARE: PLOPPY disk COMPUTER: PLO |

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Peripheral Nervous System Specific Sodium Channels, DNA Encoding Therefor, Crystallization, X-ray Diffraction, Computer Molecular Modeling, Rational Drug Design, Drug Screening, and Methods of Making and Usi
1829 DLPMVSGDRIHCLDILFAFTKAVLGDSGELDILRQQMEERFVASNPSKVSYEAYHTTERR 1888
                                              DLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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939; Conservative 266; Mismatches 397;
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                            1711 KEEEQGAAVIQRAYRKHM-----EKMVKLRLKD 1738
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48.9%; Pred. No. 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PROOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/836,325 FILING DATE: 2-MAY-1997
                                                                                                                                                                                                                 Sequence 15, Application US/08836325 Patent No. 6110672
                                                                                                                                                                                                                                                                                                Borden, Laurence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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                                                                                                                                                                                                                                                                                 Halegoua, Simon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
E: protein
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APPLICANT: Halegoua, Sir
APPLICANT: Borden, Laure
TITLE OF INVENTION: Peril
TITLE OF INVENTION: X-ra
TITLE OF INVENTION: X-ra
TITLE OF INVENTION: Drug
TITLE OF INVENTION: Ther
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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 1018 HFKQREADEVKPLDELY--EKKANCIANHTGYDIHRNGDFQKNGNGTTSGIGSSVEKYII 1075
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                                                                                                                        LRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNK-TAYA 728
                 VWDCSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIGNWV
                                                           FTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSD-NNRSFLASLRV
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Gaps

320;

| 09 | 130
119 | 190
173 | 250
232 | 305
292 | 365
350 | 424 | 459
469 | 473 | 529
487 | 589 | 528
645 | 588
699 | 647
757 | 704
810 | 763
868 | 823
926 | 879
976 | 933
1012 | 993 |
|----|---|--|--|---|---|--|-------------|--------|--|--|------------|--|---|--|--|--|---|---|--|
| :: | 11 PELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHSV 1 : | 131 FSWFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGFIVDEFSFLRD 1 | 191 PWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKKL 2 | 251 VDVMVLTLECLSIFALVGQQLFMGILNQKCIKHNCGPNPASNKDCFEKEKDSEDF 3 | 306 IMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILR 3 :: | 366 TSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEKMFGEAQQLLR- 4 :1 :: | 425EEKEALVA | RGSKTA | 470 EKLSKSSESIKKSFHLGVEGHKEKKLSTPNQSPLSIKGSLFSARRSSRTSLFSFKGRGRD 5 474 ASASDSEDD | 530 GSETEFADDEHSIFGDNESRRGSLFVPHRPERRSSNISQASRSPPLPVNGKMHSAVDCNG 5 | 488 | 529 QEQEKFQEPCFRULASKYLVWDCSPQWLCIKKVLRTIMTDFTELAITICIIINTVF 5 | 589 LAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLS- 6 :1: : : : : : : : : : : : : | 648LADVLYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLT 7 | 705 IVVFIFSVVGMRLEGTKFNKTAYATQE-RPRRRWHMDNFYHSFLVVFRILCGEWIENMWG 7
 : : : | 764 CMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLAL 8 : : : : : : : : : : : : : : : : : : | 824 DRFRRAFSFMLHALQSFCCKKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYD 8 ::: : | 880TDMALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPPETKQL 9 :: :: :: :: | 934 TSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTVSPKKQP 9 |
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                                              L-TNQAFDIIMV-LICLNMVTMMVEKEGQM------VLWINVFIILFTGECVLKLISL
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                                                                                FEDIYI-EKKTIKIILEYADKIFTYIFILEMLLKW-AYGYKTYFTNAWCWLDFLIVDV$L
                                                                                                                                         FWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQC----NISNYSWKVPQVNFD
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                                     DRCFPKGLSCHFLCH-KTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALI
                                                                       FEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSV
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CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08808793
Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT
TITLE OF INVENTION: AND USE THEREOF
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US-08-808-793-3
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                                                             -RKFFG - - SKTRKSFFMRGSKTAQA
                                                                                         ATKVRKVSTTSLSLPGSPFNLRRGSRSSHKYTIRNGRGRFGIPGSDRKPLVLQTYQDAQQ
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                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.7%; Score 3554.5;
llarity 38.4%; Pred. No. 0;
Conservative 357; Mismatches
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
                                                                                                                                      US/08/808,79
                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                           34,103
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2105 amino acids
                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                            NAME: Braman, Susan J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                     APPLICATION NUMBER:
                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
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Matches 780
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LAIVAMSYDELQKKAEEEEAAEEEAIREAEEAAAAKAAKLEERANVAAQAAQDAADAAAA
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                                                                                                                                                   38.7%; Score 3554.5;
38.4%; Pred. No. 0;
iive 357; Mismatches
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Matches 780; Conserv
                    STRANDEDNESS:
TOPOLOGY: lin
                                                                MOLECULE TYPE:
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                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
NUMBER OF SEQUENCES: 19
                                                                                                                                               1383 IAFVVIFTIECLIKVFALROHYFTNGWNLFDCVVVVLSIISTLVSR-LEDSDISFPFTLF 1441 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 | 1411 |
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                                                                KPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDILN 1382
                                                                                         KKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQD-----SCQQ 1556
                                                                                                                                                                                                                                                                                                                                                       PQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPE 1616
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CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
FIGN APPLICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,618
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
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ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Soderlund, David M. APPLICANT: Knipple, Douglas C. APPLICANT: Ingles, Patricia J.
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2105 amino acids
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REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         716-263-1636
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US-08-772-512A-3
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                                               952 IDHKDRFKDHELP--RWNFTDFMHSFMIVFRVLCGEWIESMWDCMYVGDVS--CIPFFLA 1007
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                         --NKTAYATQERPRRRWHMDNFYHSFLVVFRILCGEWIENNWGCMQDMDGSPLCIIVFVL 780
892 VLRSFRLLRVFKLAKSWPTLNLLISIMGRTMGALGNLTFVLCIIIFIFAVMGMÕLFGKNY
                                                                        IMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSF
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111 ILGPFNPLRSLMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILE 170
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8 ISEEERSLERPFTRESLLQIEQRIAEHEKQKELERKRAABGEQIRYDDEDEDEGPOPDPT 67
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                                                                                                  APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                  ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.7%; Score 3550.5;
llarity 38.4%; Pred. No. 0;
Conservative 357; Mismatches
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APPLICATION NUMBER: US 60/012,649
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                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 4, Application US/08808793
Patent No. 5858713
                                                                                                                                                                                                                                                                                                                                                                                  Eloppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   716-263-1636
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TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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779; Conserv
                                                                                                                                                                                                                                                                           Rochester
                                                                                                                                                                                                                                                                                                 New York
                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                         14603
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                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 146
RESULT 14
US-08-808-793-4
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HOUSE GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
APPLICANT: Eniple, Douglas C.
APPLICANT: Ingles, Particia J.
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: FLIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: 1463 1643 1501 1616 1676 1940 KPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDIĻN 1382 GIFVVIFSGECLLKIFALRYHYFKEPWNLFDVVVVILSILGLVLSDIIEKYFVS--PTLL 1701 IAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSR-LEDSDISFPPTLF **VVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNR** AYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQ-DIFMTEEQKKYYNAMKKLGTK RVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSWFSK[†]V PQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPE 1617 ASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGD SQCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLY KKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQD----SCQQ GFRRYFTSAWCWLDFLIVVVSVLSLM•••••NLPSLKSFRTLRALRPLRALSQFEGMK SSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKH 1727 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: LLP NIXON, HARGRAVE, DEVANS & DOYLE : P.O. Box 1051, Clinton Square Rochester Sequence 4, Application US/08772512A Patent No. 6022705 COMPUTER READABLE FORM:

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CSTIDLNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQI 1030
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                                                                          ASTMTKESKLRSRNTRNQSIGAATNGGSSTAGGGYPDANHKEQRDYEMGQDYTDEAGKIK 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2104;
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                                                                                                                                                                                                                                             19603/601 (CRFD-1657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3550.5;
Pred. No. 0;
57; Mismatches
                                                                      US/08/772,512A
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,618
FILING DATE: 01-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%; Sc
Similarity 38.4%; Pr
'9; Conservative 357;
                                                                                                                                                                                                  REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                               TELEPAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                        APPLICATION NUMBER:
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CLASSIFICATION:
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910

| δy | 1502 | 1502 KKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQDSCQQ 1556 | 1556 |
|------|--------|--|------|
| qq | 1762 | | 1820 |
| ٥y | 1557 | 1557 PQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPE 1616 | 1616 |
| QQ | 1821 | 1821 ATVGITFLLSYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDYDMYYEIWQQEDPE | 1880 |
| ογ | 1617 | 1617 ASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVWGDRLHCMDVLFAFTTRVLGD 1676 | 1676 |
| qq | 1881 | GTQYIRYDQLSEFLDVLEPPLQIHKPNKYKIISMDMPICRGDMMYCVDILDALTKDFFAR 1940 | 1940 |
| 0y | 1677 | SSGL | |
| qq | 1941 | 1941 KGNPIEETGEIGEIAARPDTEGYDPVSSTLWRQREEYCAKLIQNAWRRY 1989 | |
| | | | |
| Sear | ch com | Search completed: February 27, 2002, 01:28:58
Job time: 10148 sec | |

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4.5 Compugen Ltd. version - 2000 (GenCore Copyright (c) 1993

using sw model protein search, protein February 26, 2002, 22:49:55 Run on:

; Search time 72.7 Seconds
(without alignments)
1849.355 Million cell updates/sec

US-09-646-224A-2 9173 Title: Perfect :

.....VFCNGDLSSLDVAKVKVHND 1765 1 MEERYYPVIFPDERNFRPFT. score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | channel alp | channel | channel | channel | channel | channel alp | channel pro | channel | channel | _ | channel | _ | channel | channel | channel | channel | channel pro | channel pro | channel pro | channel | channel | channel pro | channel pro | channel | channel | S | | sodium channel pro | |
|-----------|-----------------------|-------------|---------|---------|---------|---------|-------------|-------------|---------|---------|--------|---------|--------|---------|---------|----------|---------|-------------|-------------|-------------|---------|----------|-------------|-------------|---------|---------|--------|-------|--------------------|--------|
| | Descr | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | sodium | rolta | robal | sodiur | sodium |
| SUMMARIES | | | | | | | | | | | A25019 | | | | | I54323 s | | | | | | T30902 ; | | | | | | | JC1101 s | |
| | 8 | T4238 | A33 | A38 | S5477 | 868 | A46 | 200 | A60 | B25 | A25 | CHR | 164 | 151 | 380 | 154 | 156 | CHEE | T43161 | S12 | T43 | T30 | A33 | A45 | S72 | A55 | T31 | T31 | JC1 | A60 |
| | DB | 7 | 7 | 7 | 7 | ~ | 7 | ~ | 7 | ď | ~ | ٦ | 7 | 7 | ~ | ~ | 7 | Н | ~ | 7 | 7 | N | 7 | ~ | ~ | ~ | 7 | 7 | 7 | ~ |
| | Query
Match Length | 1765 | 2019 | 2016 | 1977 | 1957 | 2005 | 1951 | 1983 | 2005 | 2009 | 1840 | 1836 | 1836 | 1836 | 1835 | 1976 | 1820 | 2049 | 2108 | 1784 | 1993 | 1820 | 1682 | 1689 | 1681 | 1699 | 1810 | 1522 | 1321 |
| op. | Query | 8.66 | 51.5 | 51.4 | 49.6 | 49.6 | 49.1 | 49.0 | 48.9 | 48.9 | 48.8 | 47.6 | 47.5 | 47.4 | 47.3 | 47.2 | 47.1 | 43.4 | 42.7 | 38.7 | 38.3 | 37.9 | 35.3 | 34.7 | 33.1 | 32.9 | 32.9 | 32.3 | 32.1 | 29.8 |
| | Score | 9157 | 4724 | 4711.5 | 4553 | 4545.5 | 4501 | 4496.5 | 4489.5 | 4484.5 | 4476 | 4363.5 | 4355.5 | 4347.5 | 4342 | 4331 | 4316.5 | 3983 | 3918 | 3554.5 | 3512 | 3479 | 3242.5 | 3184 | 3032.5 | 3021.5 | 3016.5 | 2959 | 2945 | 2732 |
| | Result
No. | 1 | ~ | ٣ | 4 | 5 | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

| sodium channel hom | voltage-gated sodi | calcium channel al | calcium channel al | voltage-dependent | dihydropyridine re | calcium channel, v | voltage-dependent | calcium channel al | voltage-dependent | calcium channel al | vol.tage-dependent | calcium channel pr | voltage-dependent | calcium channel pr |
|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| A48298 | JE0084 | 143248
T43048 | S41742 | JC5280 | A30063 | A55645 | JH0422 | A38198 | T42742 | JH0564 | A46227 | S11339 | A44467 | A45290 |
| 0 | ٥ د | 4 (3 | 7 | 7 | ~ | ~ | ~ | ~ | 7 | 7 | ~ | ~ | ~ | 7 |
| 1739 | 1695 | 1911 | 1687 | 2206 | 1873 | 1873 | 1646 | 2181 | 2203 | 2161 | 1610 | 2166 | 2139 | 2220 |
| 29.3 | 28.8 | 17.1 | 16.4 | 16.3 | 16.3 | 16.3 | 16.3 | 16.2 | 16.1 | 16.1 | 16.1 | 16.1 | 16.1 | 16.0 |
| 2686 | 2638.5 | 1566 | 1508.5 | 1499 | 1497.5 | 1495.5 | 1491 | 1484 | 1481 | 1480 | 1475.5 | 1475.5 | 1473 | 1469 |
| 30 | 31 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| RESULT 1 |
|---|
| T42388 |
| sodium channel alpha chain - rat |
| C;Species: Rattus norvegicus (Norway rat) . |
| C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 |
| C.Accession: T42388 |
| R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G. |
| Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998 |
| A:Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in perip |
| A; Reference number: Z22149; MUID:98338024 |
| A; Accession: T42388 |
| Λ;Status: preliminary; translated from GB/EMBL/DDBJ |
| A; Molecule type: mRNA |
| A; Residues: 1-1765 <dib></dib> |
| A; Cross-references: EMBL: AF059030; NID: 93372614; PID: 93372615; PIDN: AAC40199.1 |
| A; Experimental source: strain Spraque-Dawley; dorsal root ganglia |
| A; Note: preferentially expressed in sensory neurons within dorsal root ganglia and t |
| C; Superfamily: sodium channel protein |
| |

ö Gaps ; 0 2; Length 1765; Indels 1; DB Score 9157; DB Pred. No. 0; 3; Mismatches 99.88; Query Match 99.8 Best Local Similarity 99.8 Matches 1761; Conservative

61 KLPKLYGDIPPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRS 120 121 LMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGF 180 181 IVDEFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIV 240 GALLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASNKDCFEKEK 300 300 DSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLY 360 241 241 301 Karaman Karama

301 361 361

| | QLIREEKEALVAMGIDRSSLINSLOASSFSPKRRKFGSKTRKSFFMRGSKTAQASASDSE 480 |
|---|---|
| | 54 60 |
| TILKIGNWVFTGIFIAEMCLKII. | KTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDNN 660 |
| KSFLASLRVLRVFKLAKSWPTLNT
FPNKTAYATQERPRRRWHMDNFYH

:PNKTAYATQERPRRRWHMDNFYH | RSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGT 720
KFNKTAVATQERPRRWHMDNFYHSELVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVL 780
 |
| MVIGKLVVLNLFIALLLNSFSNE
 | IMVIGKLVVLNLFTALLLNSFSNBEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSF 840
 |
| CCKKCRRKNSPKPKETTESFAGEN
 | CCKKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDMALYTGQACAPLAPLAEVE 900
 |
|)DVEYCGEGGALPTSQHSAGVQAG
 | DDVEXCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRK 960
 |
| (SDAVSMLSECSTIDLNDIFRNLQ
 | KSDAVSMLSECSTIDLNDIFRNLORTVSPKRQPDRCFPRGLSCHFLCHKTDKRKSPWVLW 1020
 |
| NNIRKTCYQIVKHSWFESFIIFVII
 | WNIRKTCYOIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFL 1080
 |
| JEMILKWVAFGFRRYFTSAWCWLD | LEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLANNLPSLKSFRTLRALRPLRALSQFE 1140
 |
| BMKVVVYALISAIPAILNVLLVCL) | GMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEV 1200
 |
| NRSQCNI SNY SWKVPQVNFDNVGN
 | PNRSQCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEA 1260
 |
| ILYAYLYFUVFIIFGSFFTLNLFIC | NLVAXLYEVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLG 1320
 |
| KKPQKPIPRPLNKCQAFVFDLVTS
 | TKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDI 1380
 |
| .NIAFVVIFTIECLIKVFALRQHYF
 | LNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTL 1440
 |
| RVVRLARIGRILRLVRAARGIRTLLI
 | |
| KKGSGIDDIFNFETFTGSMLCLFQI | VKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQDSCQQPQIA 1560 |

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channel protein I, cardiac - rat
cnate names: sodium channel protein (SkM2) alpha chain
les: Rattus norvegicus (Norway rat)
130-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 20-Aug-1999
ssion: A33996; JQ0412
tt, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
watl. Acad. Sci. U.S.A. 86, 8170-8174, 1989
s: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) chan rence number: A33996; MUD:90046760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Primary structure and expression of a sodium channel characteristic of dene ence number: JQ0412; MUID:90166613 sion: JQ0412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ule type: mRNA
ues: 1-479,481-1712, T',1714-1963, R',1965-2019 <KAL>
lemental source: muscle
family: sodium channel protein
rds: cardiac muscle; duplication; heart; sodium channel; transmembrane protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                  21 IQYSALSDFADALPEPLRVAKPNKFQFLVMDLPWVMGDRLHCMDVLFAFTTRVLGDSSGL 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s: preliminary
ule type: mRNA
lues: 1-2019 <ROG>
.rrferences: GB:M27902; NID:g206857; PIDN:AAA42114.1; PID:g206858
.rrferences: Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
4, 233-242, 1990
VVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQF 1620
                                                                                   IQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGL 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 IPPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------CFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 NFRPFTSDSLAAIKKRIAIQKER-----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNC---GPNPASNKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 51.5%; Score 4724; DB 2; Length 2019; Local Similarity 50.2%; Pred. No. 0; es 976; Conservative 284; Mismatches 426; Indels 260
                                                                                                                                                                                                                                                                                                                                          SSSHQVFCNGDLSSLDVAKVKNHND 1765
                                                                                                                                                                                                                                                                                                                        SSSHQVFCNGDLSSLDVAKVKVHND 1765
                      01
                                                             61
                                                                                                                                                 21
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Feb

Wed

1119 1006 1066 1119 1059 1179 GKFGRCINGTDINMYLDFTEVPNRSQCNISNYS ----WKVPQVNFDNVGNAYLALLQVAT 1235 543 404 514 634 :| ||:||:||:||:||:||:||
DLTITMCIVLNTLFMALEHYNMTAEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQ SLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFS SLDVYLNDPANYLLKNGTTDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAWAF LAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRN VAAETEAKEKMFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSP-----KKRKFF ---RKSFFMRGSKTA-----QASASD 484 SSGTEDGGDDRLPKSDSEDGPRALNQLSLTHGLSRTSMRPRSSRGSIFTFRRRDQGSEAD 544 FADDENSTAGESESHRISLLVPWPLRHPSAQGQPGPGASAPGYVLNGKRNSTVDCNGVVS -----TKRLSQNLP-VDLFDEHVDPLHR **QRALSAVSILTITIQEQEKFQEPCFPCGKNLASKYLVWDCSPQWLCIKKVLRTIMTDPFT ELAITICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRH** GWNVFDSIVALLSLADVLYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVG ALGNLTVVLTIVVFIFSVVGMRLFGTKFNKTAYATQER---PRRRWHMDNFYHSFLVVFR ILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNE----EK DGEM-----NNLQLALARIQRGLRFVKRTTWDFCCGILRRRPKKPAALATHSQLPSCIT --NSPKPKETTESFAGENKDSILPDARPWKEYDTDMALYTGQAG--APL-APLAEVEDDV 1010 APRSPPPPEVEK------VPPARKETRFEEDKRPGQGTPGDSEPVCVPIAVAESDT EYCGE-----GGALPTSQHSAGVQAGDLPP-----ETKQLTSPDDQGVEMEVFSEE DLHLSIQSPRKKSDAVSMLSECSTIDLN---DIFRNLQKTVSPKKQPDRCFPKGLSCHFL CHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEK LLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLM-----NLP DGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCCKKCRRK-GSKT----SEDDASK --364 405 479 486 604 575 1060 950 1120 1007 1180 1067 1240 1120 1180 304 345 424 457 515 635 695 839 752 849 1300 661 721 781 897 926 904 807 Ωp Q B Qy Db 9 P qq δ 8 ò ద ò Q ò g õ õ g ç Q δ g οŽ g ò g ò oy D ò q ò g οy g

Sourtum channel protein hHI, cardiac - human
N;Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: A38195
R;Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.;
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A;Title: Primary structure and functional expression of the human cardiac tetrodotox
A;Reference number: A38195; MUID:92115699
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2016 <GELDA;Cross-references: GB:M77235; NID:9184038; PIDN:AAA58644.1; PID:9184039
A;Experimental source: heart
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle: Aniliant T-X-I human cardiac tetrodotox R.L.; transport; sodium 29; 1415 1475 1718 1648 GKFGRCINQTEGDLPLNYTIVNNKSECESFNVTGELYWTKVKVNFDNVGAGYLALLQVAT 1419 129 131 VFSMFIICTVIINCMFMANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD 183 Gaps 71 NFRPFTSDSLAAIKKRIAIQKER-----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGDI 69 PPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS VVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPS TATEESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFL YKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQ KKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGL IVLNMIIMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCV **VMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTT** Length 2016; 247; Indels DB 2; 435; 51.4%; Score 4711.5; 50.2%; Pred. No. 0; Conservative 281; Mismatches KRKEEEQGAAVIQRAYRKH-MEKMVK 1733 Query Match Best Local Similarity Matches 970; Conserv 1360 1839 1480 1416 1600 1659 1719 1649 1899 15 20 130 1420 1540 1476 1536 1709 12 1356 72 6 .B. Kutha Kutha Katha Baw oy O -6 . 60 Dp ò oy oy q 5. A 15. A ò

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
C;Accession: S54771
E;Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A;Tile: Structure and functional expression of a new member of the tetrodotoxin
A;Reference number: S54771; MUID:95237189
A;Accession: S54771
A;Accession: S5
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QAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADK 1244
                                                                         NGTDINMYLDFTEVPNRSQCNISNYS----WKVPQVNFDNVGNAYLALLQVATYKGWLEI
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Length 1977; Indels 248;

tch 49.6%; Score 4553; DB 2; I slmilarity 49.5%; Pred. No. 0; 960; Conservative 283; Mismatches 448;

Query Match Best Local S: Matches 960, S

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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Sate: 17-101-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
C;Accession: S68453
R;Akopian, A.N.; Sivilotti, L.; Wood, J.N.
Nature 379, 257-262, 1996
A;Title: A tetrodotoxin-resistant voltage-gated sodium channel expressed by A;Reference number: S68453
A;Reference number: S68453
A;Status: nucleic acid sequence not shown
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                          HSAGVQAGDLPPETKQLT----SPDDQGVE----MEVFSEEDLHLS-IQSPRKKSDAVS
                                                                    MLSECSTID--LNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIR
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A; Molecule type: mRNA
A; Residues: 1-1957 < AKO>
A; Casdues: 1-1957 < AKO>
A; Casdues: 1-1957 < AKO>
A; Cassar references: GB:192184; NID:g1209466; PIDN:CAA63095.1; PID:g1209467
A; Experimental source: dorsal root ganglia
C; Superfamily: sodium channel protein
C; Seywords: sodium channel; transmembrane protein; voltage-gated ion channel
F; 133-148/Domain: transmembrane #status predicted < TMA>
F; 225-241/Domain: transmembrane #status predicted < TMA>
F; 240-265/Domain: transmembrane #status predicted < TMA>
F; 240-265/Domain: transmembrane #status predicted < TMA>
F; 340-362/Domain: transmembrane #status predicted < TMA>
F; 36-392/Domain: transmembrane #status predicted < TMA>
F; 31-747/Domain: transmembrane #status predicted < TMA>
F; 31-747/Domain: transmembrane #status predicted < TMIO>
F; 1156-1172/Domain: transmembrane #status predicted < TMIA>
F; 1194-1210/Domain: transmembrane #status predicted < TMIA>
F; 1286-1302/Domain: transmembrane #status predicted < TMIA>
F; 1400-1416/Domain: transmembrane #status predicted < TMIA>
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F;1606-1622/Domain:
F;1708-1724/Domain:
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| Db 1655 CLFQITTSAGWDGLLSPILNTGPPYCDPNLPNSNCSRCNCGSPAVGIIFFTTVIIISFLI 1714 Oy 1575 VVNMYIAVILENEWRATEESEDPLGEDDFETFYEWWEKFDPEASOFIQYSALSDFADALP 1634 1715 VVNMYIAVILENEWRATEESEDPLGEDDFETFYEWWEKFDPEASOFIQYSALSDFADALF 1774 Oy 1635 BPLANTANILENEWRATEESEDPLGEDDFOMFYETWAKFDPEASOFIDTLS 1774 Oy 1635 BPLANTANILENEWRATEESEDPLGEDDFOMFYETWAKFDPEASOFIDTLS 1774 Oy 1635 BPLANTANILENEWRATEESOFAANIORAFRANILESSCALDFWAMPEFKEMAT 1634 Oy 1635 NDFKKLYEDIVTTTRKREEEGOCAAVIORAYRKHM 1728 1 | ૽ઌૼ૽૽૽૽ૡ૽ૺ૽ઌૼ૽૽ૡ૽ૺ૽ઌ૽ૺ૽ૡૺૹૡૼ૽૽ૡૺ૽ઌૼ૽ૹૺૡઌ૽૽૽ઌૼ૱ૡૺ૽ઌૼ૱ૡૺૡ૽ઌ૽ૺઌૺ
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| Owery Match Query Match Query Match 49.14: Score 4501; DB 2; Length 2005; Best Local Similarity 48.04: Pred; No. 0; Matches 954: Conservative 284; Mismatches 449; Indels 300; Gaps 39; Matches 954: Conservative 284; Mismatches 449; Indels 300; Gaps 39; Qy 11 PDERNERPETSDELAATKKERIAIGKERKKSKDKAARDEPREPDLEMASEKLEK 64 Qy 65 LYGDIPPELVTKPLEDLDPYTKDHYFPWINKTRIYRFSAKRALFILGPFNPLRSLMIR 124 Qy 65 LYGDIPPELVTKPLEDLDPYTKDHYFPWINKTRIYRFSAKRALFILGPFNPLRSLMIR 124 | | 955 GQTMCLTVFMMYWIGNLVVLNILFILLSSFSSDNL-AATDDDDNEMNNLQIAVGRMQKG 830 FSFMLHALQSFCCKKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDMALLY 1014 IDFVKRIREFIQKAEVRKQKALDEIKPLNKKDSCISN 886 TGQAGAPLAPLAEVDDDVEYGGGGALPTSQHSAGVOAGDLPPETKQLTSP | 1013
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| 4ZI DAVVAMAIEEQUNQAIDEEAEÇNEAEFÇQMLEQENNQQEEAQAAAAAAAASAESKUFSGAGGI | λò | 1338 FVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKY | 1397 |

| 247 LSDVMILTVFCLSVFALIGLQLFMGNLRNKCSQWPPSD-SAFETNTTSYFNGTMD 300 303 | 509 STFEDSESRRDSLFVPHRPGERRNSNGTTTETEVRKRRLSSYQISMEMLEDSSGRQRSMS 520 AVSILTITIOEOEKFOEPCGKNIASKYLVWDCSPOWLCIKKVLRTIMTDPFTELAIT | 1 1 1 1 1 1 1 1 1 1 | 975 WREYDTDMALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGD 925 1 1 1 1 1 1 1 1 1 |
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| | Db 1821 FADALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQME 1880 Qy 1689 EKFWEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRHWEKMVKLRLKDRSSSS 1743 | Suguring International processions (Norway rat) C;Species: Ratus norregicus (Norway rat) C;Species: Ratus norregicus (Norway rat) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999 C;Accession: S00320 R;Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S. FEBS Lett. 228, 187-194, 1988 A;Title: Primary structure of rat brain sodium channel III deduced from the CDNA sequence number: S00320; MuID:88137594 A;Reference number: S00320 A;Molecule type: mRNA A;Residues: 1-1971 <aarcassion a;cross-references:="" a;molecule="" c;keywords:="" c;superfamily:="" channel="" duplication;="" embl:v00766;="" mrna="" nid:957210;="" pid:957211="" pidn:caa68735.1;="" protein="" protein<="" sodium="" td="" transmembrane="" type:=""><td>Query Match Best Local Similarity 49.0%; Score 4496.5; DB 2; Length 1951; Best Local Similarity 49.0%; Pred. No. 0; Matches 945; Conservative 282; Mismatches 444; Indels 257; Gaps 36; Qy 11 PDERNFRPFTSDLAAIKRIAIOKERKEKNDK-AAEDOPROLDLKASRKLPKLYCDI 69 </td></aarcassion> | Query Match Best Local Similarity 49.0%; Score 4496.5; DB 2; Length 1951; Best Local Similarity 49.0%; Pred. No. 0; Matches 945; Conservative 282; Mismatches 444; Indels 257; Gaps 36; Qy 11 PDERNFRPFTSDLAAIKRIAIOKERKEKNDK-AAEDOPROLDLKASRKLPKLYCDI 69 |

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| **Best Local Similarity 48.5%; Pred. No. 0; atches 951; Gaps 36; matches 951; Conservative 283; Mismatches 436; Indels 291; Gaps 36; matches 951; Conservative 283; Mismatches 436; Indels 291; Gaps 36; not servative 283; Mismatches 436; Indels 291; Gaps 370; Ill | 303
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| 1205 QCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEOPDFEANL | Db 1632 KKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSAPPDCDPDAIHPGSSVKGD 1691 Qy 1554 CQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKF 1613 : : | RESULT 8 A60054 sodium channel protein IIIb, long form - rat sodium channel protein IIIb, long form - rat sodium channel protein IIIb, long form - rat c; Species Ratius norvegicus (Norway rat) C; Species Ratius norvegicus (Norway rat) C; Species Ratius norvegicus (Norway rat) C; Species Ratius 1940 # Regular 1940 C; Accession: A60054; B4824 A; Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in A; Reference number: A60054; MUID:90251117 A; Reference number: A60054 M; Molecule type: mRNA A; Rediance: 1-1983 * AOUH> A; Rochalter, K.L.; Kzzenden, D.M.; McKenna, N.M.; Caldwell, J.H. A; Rochalter, K.L.; Kzzenden, D.M.; McKenna, N.M.; Caldwell, J.H. A; Rochalter, K.L.; Kzzenden, D.M.; McKenna, N.M.; Caldwell, J.H. A; Rochalter, K.L.; Kzzenden, D.M.; McKenna, N.M.; Caldwell, J.H. A; Rochalter, K.L.; Kzzenden, D.M.; McKenna, N.M.; Caldwell, J.H. A; Rochalter, K.L.; Kzzenden, D.M.; McKenna, N.M.; Caldwell, J.H. A; Reficence number: A44824 A; Reference number: A44824 A; Reference number: A44824 A; Mole: Sequence inconsistent with the nucleotide translation A; Roches extracted from WCBI backbone (NCBIN:97388, NCBIP:97391) C; Superfamily: sodium channel protein C; Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane pr |

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Risarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
A; Description: Che EMBL Data Library, August 1991
A; Description: Developmentally regulated RNA splicing of rat brain sodium channel mR
A; Reference number: S24803
A; Reference number: S24803
A; Status: Dealinnary
A; Status: Drellinnary
A; Status: DRA
A; Residues: 183-188, 'D', 190-305 <SAR>
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C; Superfamily: sodium channel protein
C; Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltae
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48.9%; Score 4484.5;
Best Local Similarity 48.1%; Pred. No. 0;
Matches 950; Conservative 278; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-2005 <NOD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-un-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C;Accession: B25019; S24804
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.;
Nature 320, 188-192, 1986
                                                                                                                                                                                                                                                                                                                                                                                                      1289
                                                                                                                                                                                                                                                                            KPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKL 1700
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A:Reference number: A93377; WUID:86146901
                                                                                                                                                    PSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLM--
                                                                                                                                                                                                                                                                                                                                                         ELNYLKDGNGT ----TSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFEN
                                                                                           VEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTVSPKK--QPDRCFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLFDCVVVVLSIISTLVSRL-EDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFA
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-NKIDSCMSNNTG-
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                              DVEYCGEGGALPTSQHSAGVQAGD-
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Takeshima, H.; Kurasaki, M.; Takahash protein; volta rat brain sodium chan 39; Sodium channel protein I - rat
N.Alternate names: sodium channel protein A
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C.Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C.Accession: A25019; S40783; I84764
R.Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.;
Nature 320, 188-192, 1986
A.Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A.Reference number: A93377; MuID:86146901 A.Accession: I84764
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Rolecule type: mRNB
A.Rollogs: 1-2009 <RES>
A.Cross_references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089 PPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS 129 292 ETVFEFDWKSY1QDSRYHYFLEGVLDALLCGNSSDAGQCPEGYMCVKAGRNPNYGYTSFD 366 68 69 TMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHMEKMVKLRLKDRSS 1741 -- DFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFD VFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGFIVDEFSFLR LVDVMVLTLFCLSIFALVGQQLFMGILNQKCI-----KHNCGPNPAS-----N DPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKĶ PID:957217 PDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKA-AAEPQPRPQLDLKASRKLPKLYGDI Superfamily: Sodium channel protein (Keywords: duplication; ion transport; sodium channel; transmembrane Length 2009 A Accession: A25019
A; Modecule type: mRNA
B; Residues: 1-2009 <NOD5
B; Residues: 1-2009 <NOD5
B; Residues: 1-2009 on the property of the prop Indels Mismatches 444; DB 2; channel Similarity 47.9%; Score 4476; Similarity 47.9%; Pred. No. 0; 2; Conservative 289; Mismatches A; Title: Structure and function of sodium A; Reference number: I50536; MUID:87311395 A; Accession: S40783
A; Molecule type: DNA
A; Residues: 177-253 <SAR>
R; Noda, M.; Numa, S.
R; Recept. Res. 7, 467-497, 1987
A; Title: Structure and function of --KDSE--KDCFEKE--Local Simi

| QQ | 367 | | 426 |
|------------|------|--|-------------|
| δy | 399 | EKMFQEAQQLLREEKEALVAMGIDRSSLN | 442 |
| QQ | 427 | EDONQATLEBAEQKEAEFQQMLEQLKKQQEAAQQAAAATASEHSREPSAAGRLSDSSSEA | 486 |
| VQ 4 | m r | FFGSKTRKSFFWRKSFFW | 9 |
| α . | 48 | SASAKEKRAKAKAKAKEQSGGEEKUUDEFAKSESEUS | 546 |
| oy
Ob | 467 | ************************************** | 487 |
| δ | 488 | OL | 498 |
| QQ | 607 | | 999 |
| δy | 499 | NLPVDLFDE | 530 |
| οy | 531 | QEKFQEPCFKNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFLA | 290 |
| qq | 727 | LEESRQKCPPCWYKFSNIFLIWDCSPYWLKVKHIVNLVVMDPFVDLAITICIVLNTLFMA | 186 |
| λο d | 591 | VEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLAD | 650 |
| 3 |) | THE TREE WILLIAM TO THE TOTAL | 0 * 0 |
| oy
Db | 651 | V-LYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFI : | 709
903 |
| O.Y
D.D | 710 | FSVVGMRLFGTKFNKTAYATQ-ERPRRRWHMDNFYHSFLVVFRILCGEWIENNMGCMQ : | 9960 |
| γά | 9 | DMDGSPLCIIVEVLINVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRF
:: : : ::: : : : : : | |
| d
G | 961 | EVAGQAMCLTVFMMVMVIRNLVVLNLFLALLLSSFSADNL-AATDDDNEMNNLQIAVDRM | 1019 |
| λά
Q | 827 | RRAFSFMLHALQSFCCKKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDM :::: | 882
1062 |
| λά | 883 | ALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGDL | 926 |
| q | 1063 | :: : : :: : :: :: :: :: :: :: :: | 1121 |
| λĊ | 927 | PPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKT | 986 |
| q | 1122 | SDFENLNTEDFSSESDLEESKEKLNESSSSSEGSTVDIGAPAEE-OPV | 1168 |
| දු දි | 987 | VSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLMWNIRKTCYQIVKHSWFESFIIFVI 1 1 1 1 1 1 1 1 1 | 1044 |
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| දු දි | 1229 | LLSSGALIFEDVNIPSRROVEKLIRCTRONIFTFIFLEMILKWYARGERRYFTSANCWLD [| 1104 |
| 27 | 1105 | FLIVVVSVLSLMNLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPAIL | 1157. |
| q | 1289 | FLIVDVSLVSLTANALGYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIM | 1348 |
| λά | 15 | NVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQCNISNYS | 21 |
| g | 34 | NVLLVCLIFWLIFSIMGVNLFAGKFYHCVNTTTGDTF-EITEVNNHSDCLKLIERNETAR | 1407 |
| λλ | 1213 | WKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFI | 1272 |

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Species: Rattus norvegicus (Norway rat)
C.Species: No. 10007
C.Accession: JN0007
R.Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Neuron 3, 33-49, 1989
A.Title: Primary structure and functional expression of a mammalian skeletal muscle A.Reference number: JN0007; MUID:90148778
A.Accession: JN0007
A.Molecule type: mRNA
A.Residues: 1-1840 cTRI>
A.Cross-references: GB:N26643; NID:9205651; PIDN:AAA41682.1; PID:9205652
C.Comment: Action potentials propagated by skeletal muscle sodium channels are respond comment: This heavily glycosylated protein contains four homologous domains, each, C.Comment: This protein is distinct from but related to sodium channel protein is distinct from but related to sodium channel protein C.Superfamily: sodium channel protein
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                                                                                                     IFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPL 1332
                                                                                                                                                                                                                                                                                                 NKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDILNIAFVVIFTIE 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRL-EDSDISFPPTLFRVVRLARIGR 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILRLVRAARGIRTLLFALMMSLPSLFNIGLLFLVMFIYAIFGMSWFSKVKKGSGIDDIF 1511
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| Ω | 190 | DPWNWLDFSVITMAYVTEFV-DLGNISALRTFRVLRALKTITVIPGLKTIVGALIQSVK 24 | |
| > - | 4 | LECLSIFALVGQQLFMGILNQKCIKHNCGPNPASN | |
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| >- | 293 | KDSEDFIMGTWLGSR
 : :: :: :: | |
| o | 306 | NDTWNSQESWAGNSTEDWEAYINDEGNEYFLEGSNDALLCGNSSDAGHCPE 36 | |
| > - | 320 | ICDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVI 37 | , |
| ۵ | 366 | YECIKAGRNPNYGYTSYDTFSWAFLALFRLMTQDYWENLFQLTLRAAGKTYMIFFVVII | |
| >- | 380 | NLTLAVVTMAYEBQNRNVAAETEAKEKMFQEAQQLLREEKEALVAMGIDR | |
| Ω | 426 | LGSFYLINLILAVVAMAYAEQNEATLAEDQEKEEEFQQMLEKYKKHQEEL 47 | |
| >- | 4 | NSLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTKRLSQN 49 | |
| ۵ | 477 | DPTHNKDC | |
| >- | 200 | DEHVDPLHRORAL | |
| ٥ | 503 | ASGEKGPPRPSCSADSAISDAMEELEEAHQKCPPWWYKCAHKVLIWNCCAPWV 55 | |
| `~ | 260 | IDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEM 61 | |
| 0 | 260 | IIYLIVMDPFVDLGITICIVLNTLFMAMEHYPMTEHFDNVLSVGNLVFTGIFTAEM 61 | |
| 5- J | 2 0 | FRHGWNVFDSIVALLSLADV-LYNTLSDNNRSFLASLRVLRVFKLAKS | |
| 2 | N | NLIAMDFIEIFQQGWNIFDSFIVILSLVELGLANVQGLSVLKSFKLLKVFKLAKS 6/ | |
| م ج | 679 | WPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNK-TAYATQERPRRW 737
 | |
| >- | m | LCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALL 79 | |
| Ω | 737 | HSFLIVFRILCGEWIETMWDCM-EVAGQAMCLIVFLAVMVIGNLVVLNLFLALL 79 | |
| > 0 | 798 | LNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCCKKCRRK 848 1:11 | |
| >- | 849 | PKETTESFAGENKDSILPDARPWKEYDTDMAL- | |
| Ω | 841 | GLTDGPRS | |
| >- | 895 | | |
| Ω | 901 | CNFINNPYLTIQVPIASESDLEMPTEE | |
| >- | 938 | GVEMEVFSE-EDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLOKTVSPK-KOP 99 | |
| ۵ | 933 | OAFSEPEDIKKPLQPLYDGNSSVCSTADYKPPEEDPEEQAEENPEGEQP 9 | |
| >- | 994 | CPPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIF 105 | _ |
| ۵ | | ECFTEACVKRCPCLYVDISQGRGKMWWTLRRACFKIVEHNWFETFIVFMILLSSGALAF 104: | _ |
| > . | 05 | DFLIVVVSVL 111 | |
| O | 4 | DIYIEQRRVIRTILEYADKVFTYIFILEMLEKWVAYGFKVYFTNAWCWLDFLIVDVSII 110 | _ |
| . . | 1114 | SLMNLPSLKSFRTLRALRPLAALSOFEGMKVVVALISAIPAILNVLLVCLIF 1166 : | |

R; George, A.L. 31, 131-137, 1992 Ann. Neurol. 31, 131-137, 1992 Ar; Title: Primary structure of the adult human skeletal muscle voltage dependent sodify; Reference number: IS1964; MUID:92246457 A; Accession: I64893 35; 1519 1578 sodium channel alpha subunit - human C;Species: Homo sapiens (man) C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999 C;Accession: I64893 1399 1571 1631 Gaps TKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHSVFSMF 134 RPFTSDSLAAIKKRIAIQKERK--KSKDKAAAEPQPRPQLDLKASRKLPKLYGDIPPELY, 74 A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecules: 1-1836 < RES>
A; Cross-references: GB: M81758; NID: 9338212; PIDN: AAA60554.1; PID: 9338213
C; Genetics: ISCLFEITTSAGWDGLLNPILNSGPPDCDPTLENPGTNVRGDCGNPSIGICFFCSYIIS ---WKVPQVNFDN FIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDL LRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAA RGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGS MLCLFQITTSAGWDTLLNPMLEA-----KEHCNSSSQDSCQQPQIAVVYFVSYIITS VGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNL VTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDIL---NIAFVVIFTIECLIKVĖA 249; DB 2; Length 1836; Indels MEANPFKKLYEPIVTTKRKEEEQGAAVIQRAYRKH-MEKMVK 1733 WLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQCNISNYS-Query Match 47.5%; Score 4355.5; DB 2; Best Local Similarity 49.3%; Pred. No. 1.1e-315; Matches 908; Conservative 271; Mismatches 415; A;Gene: SkM1 C;Superfamily: sodium channel protein C;Keywords: duplication 1579 1692 1699 RESULT 12 1343 1400 1460 1520 1519 1572 17 1283 1400 1459 18 75 1223 1167 1223 1283 **I64893** South Office Of

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| 136 | or o | 195 | 254
254 | 292
311 | | 371 | 7 | m | 439 | 496 | 515 | 556 | 0 | 616
622 | 675 | 734 | 739 | 79 4
798 | 842
846 | 889 | 006 | 930 | 941 | 988 | 984 | 1047 | | 1104 |
|--|---|--|--|----------------------------------|---------------|------|---------|---|--|---|-----|---|---------|--|--|---|------|--|--|---|-----|--------------------------------------|---|--|--------|--|--|---|
| 7 GIPLEDLDPYYSNKKTFIVLNKGKAIFRFSATPALYLLSPFSVVRRGAIKVLIHALFSMF | S IICTVIINCMEMANSMERSFDNDIPEXVFIGIYILEAVIKILARGFIVDEFSFLR | / IMITILINCVEMIMSDPPPWSANV-ETTFTGITTFESLIKILARGFCVDDFT | 5 LDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKKLVDVM
 | 5 VLTLFCLSIFALVGQQLFWGILNQKCIKHN | 3KDSEDFIMCGTW | SNFY | GSTCDKT | 2 GYECIKTGRNPNYGYTSYDTFSWAFLALFRLMTQDYWENLFQLTLRAAGKTYMIFFVVI | 0 FLGSFYLLNLTLAVVTMAYEGONRNVAAETEAKEKMFQEAQQLLREEKEALVAMGIDRSS | SLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTK | 3 | 7 SONLEVDLFDEHVDPLHRQRALSAVSILTITIQEQEKFQEPCFPCGKNLASKYLVWDCSP
: | - Engur | 7 QWLCIKKVLRTIMTDPFTELAIFICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFI
 :: : | 7 AEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADV-LYNTLSDNNRSFLASLRVLRVFKL
 | 6 AKSWPTLNTLIKIIGHSVGALGNLTVVLITIVVFIFSVVGMRLFGTKFNK-TAYATQERPR | - 32 | 5 RRWHMDNFYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLEI | 5 ALLINSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCC | KCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDN | | LAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPP | 1 DGPPSSLELDHLNFINNPYLTIOVPIASEESDLEMPT | KQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTV- | EPEDSK | 9 PK-KQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLS : : : : : : : : | IFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWC | S GALAFEDIYIEQRRVIRTILEYADKVFTYIFIMEMLLKWVAYGFKVYFTNAWCWLDFLI |
| 7.2 | (n) | 17 | 195 | 255 | 293 | 312 | (1) | 7 | 38(| 44(| 483 | 497 | 4 | 557 | 617 | 929 | 989 | 735 | 795 | 843 | 847 | 89(| 901 | 931 | 942 | 586 | 1048 | 1045 |
| QQ | δ | 2 | Qy
Dp | Qy
Db | οy | ΩD | ογ. | g | Qy
Dp | οy | q | Qy
Dp | 3 | QY | Qy
Db | Qγ | q | Qy | 0y
0p | οy | qq | Οy | Dp | δy | qq | Qy
Dp | δy | Op |

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RESULT 13
151964
sodium channel alpha chain SCN4A, skeletal muscle - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 20-Aug-1999
C;Accession: 151964
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodi.
A;Reference number: 151964
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1836 <RES>
C;Genetics:
A;Gene: GB:SCN4A
A;Cross-references: GB:L04236; NID:9292485; PIDN:AAB59624.1; PID:9292487
C;Genetics:
A;Gene: GBB:SCN4A
A;Cross-references: GB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/C;Superfamily: sodium channel protein
C;Keywords: duplication; skeletal muscle
                                                                                                                                                                                                                                                                                1393
                                                                                                                                                                                                                                                                                                              1400
                                                                                                                                                                                                                                                                                                                                                                                                      LVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQC----NISNYSWKVP 1216
                                                                                                                                                                       FFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQ 1336
                                                                                                                                                                                                                                    SYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSA 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1580 SYIIISFLIVVNMYIAIILENFNVATEESSEPLGEDDFEMFYETWEKFDPDATQFIAYSR 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKT 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPAILNVL 1160
                                          LIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRIL 1453
                                                                                                                                                     QVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGS
                                                                                                                                                                                                                                                                                                  1337 AFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDIL--;NIAFVVIFTIEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1686 MMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHM 1728
                           AVVSVLSLM-
                                                       1105
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Gaps

Indels 249;

Query Match
47.4%; Score 4347.5; DB 2; Length 1836;
Best Local Similarity 49.2%; Pred. No. 4.3e-315;
Matches 906; Conservative 272; Mismatches 416; Indels 249;

| ٥'n | 17 | PFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASRKLPKLYGDIPPELV 7 |
|--------|-----|--|
| QQ | | RPFTRESLAAIEQR-AVEEEARLQRNKQMEIEEPERKPRSDLEAGKNLPMIYGDPPEVI 76 |
| ογ | | TKPLEDLDPYYKDHKTFWYLNKKRTIYRESAKRALFILGPFNPLRSLMIRISVHSVFSMF 134 |
| QQ | 77 | NKKTFIVLNKGKAIFRFSATPALYLL |
| οy | | IICTVIINCMFWANSMERSFDNDIPEYVFIGIYILEAVIKILARGFIVDEFSFLRDPWNW 194 |
| a
B | 137 | TILTNCVFMTMSDPPPWSKNV |
| ογ | 195 | LDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKKLVDVM 254 |
| QQ | 196 | LDFSVIMMAYLTEFV-DLGNISALRTFRVLRALKTITVIPGLKTIVGALIQSVKKLSDVM 254 |
| ογ | 255 | VLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASN |
| Dp | 255 | - <u>E</u> - |
| οý | 293 | KDSEDFIMCGTWLGSRPCPN 319 |
| Д | 312 | WYGNDSWYANDTWNSHASWATNDTFDWDAYISDEGNFYFLEGSNDALLCGNSSDAGHCPQ 371 |
| ò | 320 | GSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFVVVI 379 |
| QQ | 372 | GYECIKTGRNPNYGYTSYDTFSWAFLALFRLMTQDYWENLFQLTLRAAGKTYMIFFVVII 431 |
| δ | 380 | FLGSFYLLNLTLAVYTWAYEQNRNVAAETEAKEKMFQEAQQLLREEKEALVAMGIDRSS 439 |
| Dp | 432 | FLGSFYLINLILAVVAMAYAEQNEATLAEDKEKEEEFQQMLEKFKKHQEEL 482 |
| ογ | 440 | LNSLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTKRL 496 |
| qq | 483 | EKAKAAQALEGGEADGDPAHGKDCNGSLDTSQG 515 |
| οy | 497 | SQNLPVDLFDEHVDPLHRQRALSAVSILTITQEQEKFQEPCFPCGKNLASKYLVWDCSP 556 |
| e
G | 516 | EKGAPROSGSGDSGISDAMEELEEAHQKCPPWWYKCAHKVLIWNCCA 562 |
| ογ | 557 | OWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFI 616 |
| q | 563 | PWLKFKNIHLIVMDPFVDLGITICIVLNTLFMAMEHYPWTEHFDNVLTVGNLVFTGIFT 622 |
| ογ | 617 | AEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADV-LYNTLSDNNRSFLASLRVLRVFKL 675 |
| QQ | 623 | EMVLKLIAMDPYEYFQQGWNIFDSIIVTLSLVELGLANVQGLSVLRSFRLLRVFK |
| ٥٧ | 919 | AKSWPILNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNK-TAYATQERPR 734 |
| qq | 680 | AKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCKIALDCNL 739 |
| ογ | 735 | RRWHMDNFYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFI 794 |
| QQ | 740 | PRWHMHDFFHSFLIVFRILCGEWIETMWDCM-EVAGQAMCLTVFLMVMVIGNLVVLNLFL 798 |
| δ | 795 | ALLINSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCC 842 |
| .g | 799 | ALLLSSFSADSLAASDEDGEMNNLQIAIGRIKLGIGFAKAFLLGLLHG 846 |
| δά | 843 | KKCRRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDMALYTGQA 889 |
| qq | 847 | KILSPKDIMLSLGEADGAGEAGEGGETAPEDEKKEPPEEDLKKDNHILNHMGLA 900 |
| ٥ý | 890 | GAP |
| qq | 901 | MPTEE |
| δ | 931 | VEMEVES |
| QQ | 942 | DIFSEPEDSKKPPQPLYDGNSSVCSTADYKPPEEDPEEGAEEN 984 |

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LSDFVDTLQEPLRIAKPNKIKLITLDLPMVPGDKIHCLDILFALTKEVLGDSGEMDALKQ LVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQC----NISNYSWKVP SYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSA LSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKT PK-KQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLS SCALIFEDVNLPSRPQVEKLLRCTDNIFTFILLEMILKWVAFGFRRYFTSAWCWLDFLI FFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQ LIKVFALROHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRIL RLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSWFSKVKKGSGIDDIFNF ETFTGSMLCLFQITTSAGWDTLLNPMLEA------KEHCNSSSQDSCQQPQIAVVYFV इ. . के. . ते . के qq Ιρ ò · ŏ

RESULT

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Godium channel alpha chain - human

Godium channel alpha sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

Codecession: JS0648; A42099

Robert Bodyny: Res. Commun. 182, 794-801, 1992

Accession: JS0648; MUID: 92134303

Accession: JS0648

Accession: JS0648; MUID: 92134303

Accession: Accession:

724

832

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ISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFCRCINGTDINMYLDFTEVPNRSQC--- 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYF
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                                                                                                                                                          GLLHG------KILSPKDIMLSLGEADGAGEAGETAPEDEKKEPPEEDLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDI
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                                                                                                                                                                                                                                 ALVAMGIDRSSLNSLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQA---SASDSEDDASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MLHALQSFCCKKCRRKNSPKPKETTESF-----AGENKDSILPDAR--PWKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNHILNHMGLADGPPSSLELDHLNFINNPYLTIQVPIASEESDLE-
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Db
                                                                                 A; Molecule type: DNA
A; Residues: 1399-1312 - (ACC)
A; Residues: 1399-1312 - (ACC)
A; Residues: 1399-1312 - (ACC)
A; Cross-references: GB:SB3622; NID:9345611; PIDN:AAB21450.1; PID:9245612
A; Cross-references: CB:SB3622; NID:9345611; PIDN:AAB21450.1; PID:9245612
C; Genetics:
C; Genetics:
A; Cross-references: CB:SB125111; OMIM:170500
A; MAP position: 17423.1-17425.3
C; Soperfamily: sodium channel protein
C; Reywords: duplication; glycoprotein; phosphoprotein; transmembrane protein
C; Reywords: duplication; glycoprotein; phosphoprotein; transmembrane protein
C; Reywords: duplication; glycoprotein; predicted CTR3-
F; 119-170; Domain: transmembrane status predicted CTR3-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 4342; DB 2; Length 1836;
49.0%; Pred. No. 1.1e-314;
ive 274; Mismatches 422; Indels 250
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| 293KDCFEKE | <pre></pre> | ÓY 380 FLGSFYLLNITLAVVTMAYEEONRNVAAETEAKEKMFOEAQOLLREEKEALVAMGIDRSS 439
 | ŠY 440 LNSLQASSFSPKRRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTKRL 496 1 1 1 1 1 1 1 1 1 1 | QY 497 SONLPVDLFDEHVDPLHRQRALSAVSILTITIOEQEKFOEPCFGKNLASKYLVWDCSP 556 Db 516 EKGAPROSGSGDSGISDAMEELEEAHQKCPPWWYKCAHKVLIWNCCA 562 | OY 557 QWLCIKKVLRTIMTDPFTELAITICIIINTVPLAVEHHNMDDNLKTILKIGNWVFTGIRI 616 DD 563 PWLKFKNIHLIVMDPFVDLGITICIVLNTLEMAMEHYPMTEHFDNVLTVGNLVFTGIRT 622 | 617 AEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADV-LYNTLSDNNRSFLASLRVLRVFKL 675
 | Qy 676 AKSMPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNK-TAYATQERPR 734 | OY 735 RRWHMDNEYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLF1 794 F | Qy 795 ALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCC 842 | OY 843 KKCRKNSPKPKETTESFAGENKDSILPDARPWKEYDTDMALYTGQA 889 | CY 890 GAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPPET 930 Columbia | CY 931 KQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTV\$ 988 1 1 1 1 1 1 1 1 1 1 | QY 989 PK-KQPDRCFPKGLSCHFLCHKTDKRKSPWVLWMNIRKTCYQIVKHSWFBSFIIFVILLS 1047 | OY 1048 SGALIFEDVNLPSRPOVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLÏ 1107 [11] [1] [1] [1] [1] [1] [1] [1] [1] [1 | 1108 | 1161 | | CY 1277 FFTLNLFIGVIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQ ₁ 1336 | . 1000 |
|--|---|---|--|---|---|--|---|---|---|--|---|--|--|---|-------------|------|---|---|----------|
| | | | | | | | | | | | | <u> </u> | · 4 | <u>-</u> | | | : :: | | المدالسة |
| OY 1383 IAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFR 1442 : :: :: : : : | Qy 1443 VVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLEFLVWFIYAJFGMSWFSKVK 1502
 | OY 1503 KGSGIDDIENFETFIGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSODSC 1554 | QY 1555 QQPQIAVVYPVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFD 1614 DD 1569 GNPSIGICFFCSYIIISFLIVVNMYIAIILENFNVATEESSEPLGEDDFEMFYETWEKFD 1628 | Qy 1615 PEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVL 1674 : : | QY 1675 GDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTYRRKEEEQGAAVIQRAYRHM 1728
 | RESULT 15
1543.22 Absorb alaba cubucit - buman | change 20-Aug-1999 | **Mocratoney, A.1.; Jul, C.S.; Wang, J.; HOIIMan, E.P.; KOJas, C.; Gusella, J.F. Hum. Mol. Genet. 1, 521-527, 1992 A;Title: The genomic structure of the human skeletal muscle sodium channel gene. A;Reference number: I54323; MUID:93338444 | 6
6
6 | A.CIOSS.Telefelices: GB:LO1983; NID:933/994; FIDN:AAA/333/.1; FID:9908809
C;Genetics:
A.Gene: GDB:SCN4A.
A.Gross-references: GDB:125181; OMIM:170500
A.Man position: 1703 1-1705 | A; Introns: 91/3; 131/2; 167/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; C; Superfamily: sodium channel protein C; Keywords: duplication | Query Match 47.2%; Score 4331; DB 2; Length 1835; Best Local Similarity 49.1%; Pred. No. 7.3e-314, Matches 905; Conservative 273; Mismatches 415; Indels 250; Gaps 36; | SRK KSKDKAAAEPQPRPQLDLKASRKLFKLYGDIPPELV 74 ::: | 75 | | | OY 255 VLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASN | | |

| | 1337 AFVFDLVTSQVFDVILGLIVLNMIIMMAESADQPKDVKKTFDILNIAFVVIFTIEC 1393 | LINVTMAVETDNQSQLKVDILYNINMIFIIIFTGEC 1399 | LIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRIL 1453 | :: : : : : : | RLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFGMSWFSKVKKGSGIDDIFNF 1513 | RIRGAKGIRTLLFALMMSLPALFNIGLLFLVMFIYSIFGMSNFAYVKKESGIDDMFNF 1518 | | ETFGNSIICLFEITITSAGWDGLLNPILNSGPPDCDPNLENPGTSVKGDCGNPSIGICFFC 1578 | SYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQFIQYSA 1625 | FNVATEESSEPLGEDDFEMFYETWEKFDPDATQFIAYSR 1638 | 1626 LSDFADALPEPLRVAKPNKFQFLVMDLPWVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKT 1685 | LSDFVDTLQEPLRIAKPNKIKLITLDLPMVPGDKIHCLDILFALTKEVLGDSGEMDALKQ 1698 | TTKRKEEEGGAAVIORAYRKHM 1728 | TLKRKHEEVCAIKIQRAYRRHL 1741 | |
|------|--|---|---|-----------------------------------|---|---|------|--|---|--|--|---|---|-----------------------------|--|
| | AFVFDLVTSQVFDVIILGLIVLNM | GMVYDLVTKQAFDITIMILICLNM | | VLKMLALRQYYFTVGWNIFDFVVV | | | | | | | LSDFADALPEPLRVAKPNKFQFLVN | LSDFVDTLQEPLRIAKPNKIKLIT | 1686 MMEEKFMEANPFKKLYEPIVTTKRKEEEQGAAVIQRAYRKHM | TMEEKFMAANPSKVSYEPITTTK | |
| 1284 | 1337 | 1343 | 1394 | 1400 | 1454 | 1459 | 1514 | 1519 | 1566 | 1579 | 1626 | 1639 | 1686 | 1699 | |
| QQ | Qy | qq | ٥y | qq | Qγ | qq | Οy | QQ | Qy | qq | Qy | QQ | Οy | qq | |

Search completed: February 27, 2002, 01:30:22 Job time: 9627 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 27, 2002, 01:29:01 ; Search time 67.45 Seconds (without alignments) 959.428 Million cell updates/sec Run on:

US-09-646-224A-2

1 MEERYYPVIFPDERNFRPFT.......VFCNGDLSSLDVAKVKVHND 1765 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|--------|--------|-------|--------|----------|------------|--------------------|
| Result | | Query | | | | • |
|
Q | Score | Match | Length | - BB | ID | Description |
| 1 | 4724 | 51.5 | 2019 | 7 | CIN5_RAT | F |
| 7 | 4711.5 | _ | 2016 | | CINS_HUMAN | Q14524 homo sapien |
| Э | 4502 | σ | 2002 | Н | CIN2_HUMAN | Omod (|
| 4 | 4496.5 | 49.0 | 1951 | П | CIN3_RAT | rattu |
| S | 4496 | 49.0 | 2009 | Н | CIN1_HUMAN | P35498 homo sapien |
| 9 | 4493.5 | 49.0 | 1951 | - | CIN3_HUMAN | 9 ошо |
| 7 | 4484.5 | 48.9 | 2005 | Н | CIN2_RAT | 5 rattu |
| 80 | 4476 | 48.8 | 2009 | - | CIN1_RAT | P04774 rattus norv |
| σ | 4363.5 | 47.6 | 1840 | Н | CIN4_RAT | 33 |
| 10 | 4347.5 | 47.4 | 1836 | | CIN4_HUMAN | σ. |
| 11 | 3983 | 43.4 | 1820 | ~ | CINA_ELEEL | _ |
| 12 | 3524.5 | | 2131 | | CINA_DROME | |
| 13 | 3184 | 4 | 1682 | H | CIN6_HUMAN | |
| 14 | 2945 | 32.1 | 1522 | Н | CIN1_LOLBL | |
| 15 | 1508.5 | 16.4 | 1687 | - | CCAM_MUSDO | Q25452 musca domes |
| 16 | 1497.5 | 16.3 | 1873 | | CCAS_RABIT | |
| 17 | 1496 | 16.3 | 1873 | - | CCAS_HUMAN | homo sa |
| 18 | 1482 | 16.2 | 2190 | | CCAD_CHICK | |
| 19 | 1481 | 16.1 | 2203 | ~ | CCAD_RAT | rattus |
| 20 | 1478 | 16.1 | 1835 | Н | CCAI_RAT | |
| 21 | 1475.5 | 16.1 | 1610 | - | CCAD_MESAU | Q99244 mesocricetu |
| 22 | 1473 | 16.1 | 2139 | - | CCAC_MOUSE | - |
| 23 | 1472 | 16.0 | 2161 | - | CCAD_HUMAN | 3 homo |
| 24 | 1469 | 16.0 | 2221 | - | CCAC_HUMAN | |
| 25 | 1460 | 15.9 | 1852 | - | CCAS_CYPCA | |
| 56 | 1456 | 15.9 | 2171 | - | CCAC_RABIT | - |
| 27 | 1453 | 15.8 | 2212 | - | CCAA_RAT | ^, |
| 28 | 1452 | 15.8 | 2326 | - | CCAB_DISOM | P56698 discopyge o |
| 29 | 1448.5 | 15.8 | 2169 | Н. | CCAC_RAT | ٠. |
| 30 | 1443 | 15.7 | 2516 | ~4 | CCAD_DROME | Q24270 drosophila |
| 31 | 1439.5 | 15.7 | 1966 | П | CCAF_HUMAN | 340 homo |
| 32 | 1438 | 15.7 | 2272 | - | CCAE_MOUSE | 1290 |
| 33 | 1437.5 | 15.7 | 2223 | Η. | CCAE_DISOM | P56699 discopyge o |

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VARIANTS LQT3.
WEDLINE-95196273; PubMed-7889574;
Wang Q., Shen J., Splawski I., Atkinson D., Li Z., Robinson J.L.,
Moss A.J., Towbin J.A., Keating M.T.;
"SCNSA mutations associated with an inherited cardiac arrhythmia, long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNPMLE-AKEHC-----NSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFN 1588
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                                VVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92115699; PubMed-1309946; Gellens M.E., George A.L. Jr., Chen L.Q., Chahine M., Horn R., Gallens M.E., Kallen R.G.; Estrain R.G.; Estr
YKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQ
                                                                                                                                                       KKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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VARIANTS LOT3.
WEDLINE-95081224; PubMed-8541846;
WEDG. Shen J. Li Z., Timothy K., Vincent G.M., Priori S.G.,
Schwartz P.J., Keating M.T.;
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20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE ALPHA-SUBUNIT (HH1).
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George A.L. Jr.; "Congenital long-OT syndrome caused by a novel mutation in a conserved acidic domain of the cardiac Na+ channel.";
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     "Cardiac sodium channel mutations in patients with long QT syndrome, an inherited cardiac arrhythmia.";
Hum. Mol. Genet. 4:1603-1607(1995).
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Yamagishi H., Furutani M., Kamisago M., Morikawa Y., Kojima Y.,
Hino Y., Furutani Y., Kimura M., Imamura S.-I., Takao A., Momma
Matsuoka R.;
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Benhorin J., Goldmit M., Maccluer J.W., Blangero J., Goffen R.
Lelbovitch A., Rahat A., Wang Q., Medina A., Towbin J., Kerem
"Identification of a new SCNSA mutation, D1840G, associated wi
                                                                                                                                                                                                                                                                                       MEDLINE=98349542; Pubmed=9686753;
An R.H., Wang X.L., Kerem B., Benhorin J., Medina A., Goldmit
Kass R.S.;
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Wei J., Wang D.W., Alings M., Fish F., Wathen M., Roden D.M.,
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MEDLINE-98165676; PubMed-9506831;
Makita N., Shirai N., Nagashima M., Matsuoka R., Yamada Y.,
                                                                                                                                                                    Bennett.P.B., Yazawa K., Makita N., George A.L. Jr.;
"Molecular mechanism for an inherited cardiac arrhythmia.";
                                                                                                                                                                                                                                                                                                                                                                                      "Novel LOT-3 mutation affects Na+ channel activity through interactions between alpha- and betal-subunits."; Circ. Res. 83:141-146(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A de novo missense mutation of human cardiac Na(novel molecular mechanisms of long QT syndrome."; FEBS Lett. 423:5:9(1998).
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95379949; PubMed-7651517;
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FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES, ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN PORMS A SODIUM-SELECTIVE CHANNEL TRROUGH WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL CHANNEL IS RESPONSIBLE FOR THE INTITAL UPSTROOF THE STROPORY. THIS PRESPONSIBLE FOR THE INTITAL UPSTROKE OF THE ACTION

KCNE1, and KCNE2."; Circulation 102:1178-1185(2000).

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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN HUMAN ATRIAL AND VENTRICULAR
CARDIAC MUSCLE BUT NOT IN ADULT SKELETAL MUSCLE, BRAIN,
MYOMETRIUM, LIVER, OR SPLEEN.
-!- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS ($1,$2,$3,$5,$6) AND ONE POSITIVELY CHARGED
SEGMENT ($4). SEGMENTS ($1,$2,$3,$5,$6) AND ONE POSITIVELY CHARGED
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION
-!- DISEASE: DEFECTS IN SCN5A ARE THE CAUSE OF LONG QT SYNDROME TYPE 3
(LQT3), AN AUTSOOMAL DOMINANT CARDIAC DISEASE CHARACTERIZED BY
RECURRENT SYNCOPE AND SUDDEN CARDIAC DEATH.
-!- MISCELLANBOUS: NA - CHANNELS IN MAMMALIAN CARDIAC MEMBRANE HAVE
FUNCTIONAL PROPERTIES QUITE DISTINCT FROM NA+ CHANNELS IN NERVE
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SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
SIMILARITY: CONTAINS 1 TO DOMAIN.
DATABASE: NAME-LQTSdb; NOTE-SCN5A mutations page;
WWW-"http://www.ssi.dk/en/forskning/lqtsdb/scn5a.htm".
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Glycoprotein; Repeat; Multigene family; Phosphorylation;
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InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR001698; IQ.
InterPro: IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
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1715 1903 Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEMBABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL channel o o Masmuth J.J. α MGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKRKEEBQ DPLGEDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMV Euteleostomi; u C.-M., Han J., Rado T.A., Brown G.B.; Differential expression of two sodium channel subtypes in human segment) gene is o Ö functional human brain. Brown Ferrer-Montiel for human brain sodium Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo. SEQUENCE OF 1702-1772 FROM N.A.
MEDLINE=91110524; PubMed=1846440;
Han J., Lu C.-M., Brown G.B., Rado T.A.;
"Direct amplification of a single dissected chromosomal polymerase chain reaction: a human brain sodium channel chromosome 2q22-q23."; S.D., Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-M Schinder A.F., McPherson J.D., Wagner-Mcpherson C.B., sodium channel from 89:8220-8224(1992). Schade Last sequence update)
Last annotation update)
W, BRAIN II ALPHA SUBUNIT. 2005 AA M.L., Lu C.-M., Eichelberger J.S., Beckman "Isolation of the S'-flanking region subtype II alpha-Subunit (SCN2A)."; PRT; MEDLINE=92390418; PubMed=1325650; TISSUE=Brain; MEDLINE=92275082; PubMed=1317301; chromosomal SEQUENCE OF 1702-2005 FROM N.A. CIN2_HUMAN STANDARD; 099250; 014472; 01-JUN-1994 (Rel. 29, Created) 30-MAY-2000 (Rel. 39, Last seq 20-AUG-2001 (Rel. 40, Last ann Evans G.A., Montal M.;
"Primary structure, chromosoma
"Pression of a voltage-gated
Proc. Natl. Acad. Sci. U.S.A. Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; FEBS Lett, 303:53-58(1992) SEQUENCE OF 1-89 FROM N.A. SODIUM CHANNEL PROTEIN, SCN2A1 OR SCN2A OR NAC2. GAAVIQRAYRKHM 1728 1904 SAMVIQRAFRRHL 1916 Homo sapiens (Human) SEQUENCE FROM N.A. NCBI_TaxID=9606; TISSUE-Brain; Mammalia; brain. CIN2_HUMAN 1716 1596 1784 1656 RESULT

CHARGED

2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGES SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND 1 CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT SUMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

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SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE

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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                transport; Voltage-gated channel;
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InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001685; Channel_pore_Ca_Na.
InterPro: IPR001696; Na_channel.
Pfan; PF00520; ion_trans; 4.
Pfan; PF00612; IQ; 2.
PRINTS; PR00170; NACHANNEL.
SMART; SM00015; IQ; 1.
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K -> R (IN REF. 3 AND 4).
DKGKDIRESKK -> VEKIKKPFTK (IN REF. 3).
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Matches 954; Conservative 284; Mismatches 449;
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                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 WITOROPHOBLIC SEGMENTS (SI.52,53,55,56) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED ANINO ACIDS AT
                                                         01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM CHANNEL PROTEIN, BRAIN III ALPHA SUBUNIT (VOLTAGE-GATED SODIUM
                                                                                                                                                                                                                                                                                                                              PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                Rattus.
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                                                                                                                                                                                                                                                      Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
"Primary structure of rat brain sodium channel III deduced from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transport; Voltage-gated channel;
                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVERY THIRD POSITION.
-!- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
-!- SIMILARITY: CONTAINS 1 1Q DOMAIN.
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InterPro; IPR001636; Cation_chan_non_lig-
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR000048; IQ.
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MEDLINE-88137594; PubMed-2449363;
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Pfam; PF00520; ion_trans; 4.
Pfam; PF00612; IQ; 1.
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                                           01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                  228:187-194(1988)
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               STANDARD;
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
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401
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FEBS Lett. 228:3
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              CIN3_RAT
P08104;
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CIN3_RAT
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QCN1--SNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANL 1262 RVVRLARIGRILRLVRAARGIRFLLFALMASLPSLFNIGLLLELVMFIYAIFGMSWFSKV 1501 ||:||||||||||||||||| RVIRLARIGRILRLIKGAKGIRFLLFALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYV 1631 FRRYFTSAWCWLDFLIVVVSVLSLM-----NLPSLKSFRTLRALRPLRALSQFEGMKV 1144 757 KVQLALDRFRRAFSFMLHALQSFCCKKCRRK---NSPKPKETTESFAGENKDS1LPDARP DCQALGKQARWKNVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPIYEENL YAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTK KPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDILN IAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRL-EDSDISFPPTLF LVFIVLFTGEFLLKLISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS--PTLF ICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVF DSIVALLSLADV-LYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGN LIVVLTIVVFIFSVVGMRLFGTKFNK-TAYATQERPRRRWHMDNFYHSFLVVFRILCGEW IENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKT IDLNDIFRNLQKTVSPKK - - QPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIV VVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRS STFEDSESRRDSLFVPHRPGERRNSNGTTTETEVRKRRLSSYQISMEMLEDSSGRQRSMS WKEYDTDMALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGD----------LPPETKQLTSP-----DDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECST

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SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS ($1,$2,$3,$5,$6) AND ONE POSITIVELY CHARGED SEGMENT ($4). SEGMENTS $4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE EVERY THIRD POSITION.
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   ----HCNSSSQDS 1553
                 FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N., Li X., Jabs E.W., Korenberg J.R., Ingram V.M.; "Localization of a putative human brain sodium channel gene (SCNIA)
                                                                                CGNPSVGIFFFVSXIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEKF
                                                                                                                                                  COOPOIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKF
                                                                                                                                  DPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRV
                                                                                                                                                                                                LGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHMEKMVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Chaigne D.,
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MEDLINE-92275082; PubMed-1317301;
Lu C.-M., Han J., Rado T.A., Brown G.B.;
"Differential expression of two sodium channel subtypes in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An-Gourfinkel I., Brice A., LeGuern E., Moulard B., Chaigne D., Burest C., Malafosse A.;
"Mutations of SCNIA, encoding a neuronal sodium channel, in two families with GEFS+2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS GEFS+2 MET-875 AND HIS-1648. MEDLINE-20206553; PubMed-10742094; Escayg A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld
   KKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKE----
                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Last sequence update) SODIUM CHANNEL PROTEIN, BRAIN I ALPHA SUBUNIT. SCNIA OR SCHI OR NACI.
                                                                                                                                                                                                                                                                                                                                                                                  2009 AA
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P35498 Q16172;
D1JUN-1994 (Rel. 29, Created)
20-AUG-2001 (Rel. 40, Last seq.
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SEQUENCE OF 1335-1428 FROM N.A.
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FEBS Lett. 303:53-58(1992)
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1869 QRLKNISS 1876
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                        DISEASE: DEFECTS IN SCNIA ARE THE CAUSE OF GENERALIZED EPILEPSY WITH FEBRILE SEIZURE PLUS TYPE 2 (GENE4-2). THIS AUTOSONAL DOMINANT DISORDER IS CHARACTERIZED BY FEBRILE SEIZURES IN CHILDREN AND AFEBRILE SEIZURES IN ADULTS. PENETRANCE IS INCOMPLETE AND A LARGE INTRAFAMILIAL VARIBBILITY OF THE PHENOTYPE IS OBSERVED. SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00520; ion_trans; 4.
Pfam; PF00612; IQ; 2.
SMART; SM00015; IQ; 1.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
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PIR: $22184; $22184.
MIM: 182389; -.
MIM: 604233; -.
InterPro: IPR0005111; Cat_channel_TrpL
InterPro: IPR000568; CatLon_chan_non_
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InterPro: IPR000048; IQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE. SUBGLELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: 2 ISOPORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS ($1,$2,$3,$5,$6) AND ONE POSITIVELY CHARGED SEGMENT ($4). SEGMENTS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.; "Cloning, distribution and functional analysis of the human brain type III sodium channel from human brain."; submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of endogenous currents by stable transfection of the Beta 1
                                                                                                                                                                                                   09NY46: 09Y6P4; 09UPD1; 016142; 09NX42;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM CHANNEL PROTEIN, BRAIN III ALPHA SUBUNIT (VOLTAGE-GATED SODIUM CHANNEL SUBTYPE III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolation of a human-brain sodium-channel gene encoding two isoforms of the subtype III alpha-subunit.", Mol. Neurosci. 10:67-70(1998).
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-!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFEMANTIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malo M.S., Srivastava K., Andresen J.M., Chen X.N., Korenberg J.R., Ingram V.M.;
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1876 LGESGEMDALRIQMEERFMASNPSKVSYQPITTTLKRKQEEVSAVIIQRAYRRHLLK 1932
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).
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SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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(See http://www.isb-sib.ch/announce/
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InterPro, IPR001682; Channel_pore_Ca_Na.
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requires a license agreement (
an email to license@isb-sib.ch)
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InterPro; IPR001696; Na_channel.
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                                                                                       AF035685; AAC29514.1; -. AF035686; AAC29515.1; -. S69887; AAB30530.1; -.
                                                                   EMBL; AJ251507; CAB85895.1; -.
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PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                                                                                                          SEQUENCE FROM N.A. MEDITHE-86146901; PubMed=3754035; Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M., Takahashi H., Numa S.; "Existence of distinct sodium channel messenger RNAs in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                         Nature 320:188-192(1986).
-i- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
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SUBGINIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
SEMENTY: TO OTHER SODIUM CHANNEL PROTEINS.
SIMILARITY: COUTAINS 1 1Q DOMAIN.

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InterPro; IPR002111; Cat_channel_TrpL. InterPro; IPR000636; Cation_chan_non_lig. InterPro; IPR001682; Channel_pore_Ca_Na. InterPro; IPR000048; IQ InterPro; IPR001696; Na_channel Pfam; PF00520; ion_trans; 4. Pfam; PF00612; IQ; 1. PR00170; NACHANNEL. EMBL; X03639; CAA27287.1; B25019; B25019 SM00015; PRINTS; SMART;

PROSITE: PSS0096; IQ; 1.
Ionic channel: Transmembrane: Ion transport: Voltage-gated channel; REPEAT Multigene family 1 456 I. 1294 1320 1367 1473 1473 1585 1585 1527 1562 1592 Glycoprotein; **TRANSMEM FRANSMEM FRANSMEM** TRANSMEN PRANSMEN TRANSMEM PRANSMEM TRANSMEM FRANSMEN **TRANSMEN** FRANSMEN **TRANSMEM** REPEAT REPEAT REPEAT REPEAT

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Gaps Length 2005; Indels 301; Score 4484.5; DB 1; Pred. No. 1.8e-276; Mismatches Conservative 278; 48.98; 48.18; Query Match Best Local Similarity Matches 950; Conserv

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65 IYGDIPPEMVSEPLEDLDPYXINKKTFIVLNKGKAISRFSATSALXILTPFNPIRKLAIK 124 LYGDIPPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIR 124 64 64 PDERNFRPFTSDSLAAIKKRIAIQK - - - - - ERKKSKDKAAAEPQPRPQLDLKASRKLPK 6 11 65

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243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQW-----PPDNSTFEINITSFFN

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433 387 NLTLAVVTMAYEEQNRNVAAETEAKEKMFQE-AQQLLREEKEALVAM-------LNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLL 328

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REPEAT REPEAT

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                                                                   AVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLA
                                                                                                 DV-LYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVF
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                                                                                                                                                                                                                      MALYTGQAGAPLAPLAEVEDDVEYCGEG----GALPTSQHSAGVQAGD----LPPETKQL
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus. Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M., Takahashi H., Numa S.; "Existence of distinct sodium channel messenger RNAs in rat brain."; Nature 320:188-192(1986). 13-AUG-1987 (Rel. 05, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) SODIUM CHANNEL PROTEIN, BRAIN I ALPHA SUBUNIT 2009 AA [1]
SEQUENCE FROM N.A.
MEDLINE=86146901; Pubmed=3754035; SEQUENCE FROM N.A. MEDLINE-87311395; PubMed-2442385; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequ 20-AUG-2001 (Rel. 40, Last anno Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; STANDARD; Rattus norvegicus (Rat). NCBI_TaxID=10116; CIN1_RAT P04774;

PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL Noda M., Numa S.;
"Structure and function of sodium channel.";
J. Recept. Res. 7:467-497(1987).
-I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION GRADIENT

SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 SEGMENTS (S.1.52, S3.55, S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT

EVERY THIRD POSITION.
SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
SIMILARITY: CONTAINS 1 IQ DOMAIN.

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Cation_chan_non_lig.
Channel_pore_Ca_Na. EMBL; X03638; CAA27286.1; -. InterPro; IPR002111; InterPro; IPR000636; PIR; A25019; A25019. EMBL;

IQ. Na_channel.

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family. | transport; Voltage-gated channel; | | 293 KDCFEKEK |
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CARBOHYD 301 | 295 N-L
301 N-L | INKED (GLCNAC. | | 3 ~ S | |
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1378 N-L | INKED (GLCNAC. | | q _e e | 904 FAVVGMOLFGKSY |
| FT | CARBOHYD 1392
CARBOHYD 1403 | 1392 N-L
1403 N-L | -LINKED (GLCNAC | | ÖŻ | 767 DMDGSPLCIIVFV |
| ÖS | SEQUENCE 2009 A. | A; 228769 MW; | 6808466F6368. | B | q ₁ | |
| ÕÄ | Query Match 48.8% Best Local Similarity 47.9% | | Score 4476; DB 1
Pred, No. 6.2e-27 | 3 1; Length 2009;
276; | ÇY
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| qα | 129 LFSMLIMCTILT | NCVEMTMSNPPDWTK | NV-EYTFTGIYTFI | ESLIKIIARGFCLEDFTFLR 187 | | |
| ò | 190 DPWNWLDFIVIG | DPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAI | ALRTERVERALKA: | SVISGLKVIVGALLRSVKK 24 | | |
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442 466 726 650 846 926 487 909 498 999 530 'VLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRF 826 292 306 338 QGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKT -----KHNCGPNPAS-----N KDSE-----DFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFD AKEKMFQEAQQLLREEKEAL - - - - - - - VAMGIDRSSLNS -----AQASASDSEDDASKNP ---LEQTKRLS-----0 ANSNI, SQTSRSSRMI, AGI, PANGKMHSTVDCNGVVSI, VGGPSVPTSPVGQ SFCCKKCRKKNSPKPKETTESFAGENKDSILPDARPWKEY - - - - DTDM APLAEVEDDVEYCGEGGAL------PTSQHSAGVQAGDL --FFGSKT-----RKSFFM------SIFALVGQQLFMGILNQKCI---------RGSKT-----

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle sodium channel.";
Neuron 3:33-49(1899).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT. THIS SODIUM CHANNEL MAY BE PRESENT IN BOTH DENERVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trimmer J.S., Cooperman S.S., Tomiko S.A., Zhou J., Crean S.M., Boyle M.B., Kallen R.G., Sheng Z., Barchi R.L., Sigworth F.J., Goodman R.H., Agnew W.S., Mandel G.; Primary structure and functional expression of a mammalian skeletal
                                                                                                                                                                                 IFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPL
                                                                                                                     NVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQC-----NISNYS
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20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (MU·1).
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SEQUENCE FROM N.A.
MEDLINE=90148778; PubMed=2559760;
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        SUBUNIT: MUSCLE SODIUM CHANNELS CONTAIN AN ALPHA SUBUNIT AND A SMALLER BETA SUBUNIT.
SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN,
HYDROPHOBIC SEGMENTS (31,52,53,55,56) AND ONE POSITIVELY CHARGED SEGMENT (54). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARGED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT SUMMER THIRD POSITION.
SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
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Phosphorylation.
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InterPro; IPR000636; Cation_chan_non_lig.
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Pfam; PF00612; IQ; 1.
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InterPro; IPR000048;
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PHOSPHORYLATION (BY CAPK)

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                                      PLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPPETKQLTSPD
                                                                                                           DQGVEMEVFSE-EDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTV--SPK-KQP
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MEDLINE-93265141; PubMed-1338909; MCCLatchey A.I., McKenna Yasek D., Cros D., Worthen H.G., Kuncl R.W., Desilva S.M., Cornblath D.R., Gusella J.F., Brown R.H. Jr., "Novel mutations in families with unusual and variable disorders of the skeletal muscle sodium channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ptacek L.J., George A.L. Jr., Barchi R.L., Griggs R.C., Riggs J.E., Robertson M., Leppert M.F.;
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                                                                                                      "Sequence and genomic structure of the human adult skeletal muscle sodium channel alpha subunit gene on 17q."; Biochem. Biophys. Res. Commun. 182:794-801(1992).
                                                                                                                                                                                                 genomic structure of the human skeletal muscle sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Temperature-sensitive mutations in the III-IV cytoplasmic loop region of the skeletal muscle sodium channel gene in paramyotonia congenita.";
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  R., Kallen R.G.,
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subunit in hyperkalaemic periodic paralysis.";
Nature 354:387-389(1991).
                                                                                                                                                                                                                                                         TISSUE=Skeletal muscle;
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Barchi R.L., Robertson M., Leppert M.F.;
"Identification of a mutation in the gene causing hyperkalemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92154689; PubMed-1310898;
McClatchey A.I., van den Bergh P., Pericak-Vance M.A., Raskind
Verellen C., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
Brown R.H. Jr., Gusella J.F.;
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                                                                                                                                                              MEDLINE-93338444; PubMed-1339144;
McClatchey A.I., Lin C.S., Wang J., Hoffman E.P., Rojas C.V.,
                                                           MEDLINE-92134303; PubMed-1310396;
Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas
Hoffmann E.P.;
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8:891-897(1992).
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VARIANTS PMC CYS-1448 AND HIS-1448.
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MEDLINE-93270429; PubMed-8388676;
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MEDLINE=92065978; PubMed=1659668;
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                                                                                                                                                                                                                        Mol. Genet. 1:521-521(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92265302; PubMed=1316765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genet. 2:148-152(1992).
                                                                                                                                                                                                                                                                                                                                                                                                   periodic paralysis.";
Cell 67:1021-1027(1991).
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                                                                                                                                          [2]
SEQUENCE FROM N.A.
                                                        SEQUENCE FROM N.A. MEDLINE-92134303;
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SEQUENCE FROM N.A.
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Variant met-704.
                                  NCBI_TaxID=9606;
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Ptacek L.J., Gouw L., Kwiecinski H., McManis P., Mendell J.R.,
Barohn R.J., George A.L. Jr., Barchi R.L., Robertson M., Leppert M.F.;
"Sodium channel mutations in paramyotonia congenita and hyperkalemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96154961: PubMed-8580427;

Koch M.C., Baumbach K., George A.L., Ricker K.;

Koch M.C., Baumbach K., George A.L., Ricker K.;

Koch M.C., Baumbach K., George A.L., Ricker K.;

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-! FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t
                                                                                                                                                                                                                                                                                              MEDLINE=94141728; PubMed=8308722; Lecthe H., Heine R., Pika U., George A.L. Jr., Mitrovic N., Browatzki M., Weiss T., Rivet-Bastide M., Franke C., Lomonaco M., Ricker K., Lehmann-Horn F.; Hwan soddium channel myotonia: slowed channel inactivation due to substitutions for a glycine within the III-IV linker."; J Physiol. (Lond) 470:13-22(1993).
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Heine R., Pika U., Lehmann-Horn F.;
"A novel SCN4A mutation causing myotonia aggravated by cold and
                                                                                                                                                                                                                                                           VARIANTS PMC ALA-1306; GLU-1306 AND VAL-1306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Genet. 2:1349-1353(1993).
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SUBBUNIT: MUSCLE SODIUM CHANNELS CONTAIN AN ALPHA SUBUNIT AND A SMALLER BETA SUBUNIT.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (31, 22, 33, 25, 56) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS 54 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT. THIS SODIUM CHANNEL MAY BE PRESENT IN BOTH DENERVATED AND INNERVATED SKELETAL MUSCLE.

EVERY THIRD POSITION.

DISEASE: DEFECTS IN SCN4A ARE THE CAUSE OF BOTH HYPERKALEMIC DISEASE: DEFECTS IN SCN4A ARE THE CAUSE OF BOTH HYPERKALEMIC BRENOUT PARLYSIS (HYPP) AND PARAMYOTONIA CONGENITA (PMC) WHICH ARE NOW BOTH KNOWN AS SODIUM CHANNEL DISEASE. CHARACTERIZED BY MUSCLE STIFFNESS DUE TO MEMBRANE HYPEREXCITABILITY. SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

SIMILARITY: CONTAINS 1 1Q DOMAIN.

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L01983; AAA75557.1; ALT_SEQ. L01962; AAA75557.1; JOINED. JOINED.
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FFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQ 1336
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                                       GSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVI
                                                                             FLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEKMFQEAQQLLREEKEALVAMGIDRSS
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47.4%; Score 4347.5; DB 1
Best Local Similarity 49.2%; Pred. No. 7.8e-268;
Matches 906; Conservative 272; Mismatches 416;
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InterPro; IPR001682; Channel_pore_Ca_Na.
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DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 YEADROPHOBALC SEGMENTS (S1,52,53,55,56) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS 34 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                       1400
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- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primary structure of Electrophorus electricus sodium channel deduced
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Electrophorus electricus (Electric eel).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii: Teleostei; Euteleostei; Ostariophysi;
Gymnotiformes; Electrophoridae; Electrophorus.
NCBI_TaxID=8005;
                                                                                                                                                                                                                                                                                                                                                                                                                                            GMYYDLVIKQAFDITIMILICLNMYTMWVETDDQS---QLKYDILYNINMIFIIIFTGEC
                                                                                                                                                                                                                                                                                                                             AFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTFDIL---NIAFVVIFTIEC
                                                                                                                                                                                 LIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFRVVRLARIGRIL
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MEDLINE-85061498; PubMed-6209577;
Noda M., Shimizu S., Tanabe T., Takai T., Kayano T., Ikeda T.,
Takahashi H., Nakayama H., Kanaoka Y., Minamino N., Kangawa K.,
Matsuo H., Kattery M.A., Hirose T., Inayama S., Hayashida H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVERY THIRD POSITION.
MISCELLANEOUS: AVAILABLE DATA SUGGEST THAT ACTIVATION AND
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Last annotation update)
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01, Last seq
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   INACTIVATION GATES ARE LOCATED NEAR THE CYTOPLASMIC SURFACE OF THI
MEMBRANE. IT IS HYPOTHESIZED THAT RESIDUES 802-806, 847-857,
894-910, AND 942-955 MIGHY, IN CONJUNCTION WITH THE POSITIVELY
CHARGED RESIDUES OF 84, ACT AS A VOLTAGE SENSOR INVOLVED WITH THE
                                                                                                                                                                                                                                                                                                                                    Pfam; PF00520; ion_trans; 4.
PRINTS; PR00170; NACHANNEL.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON PROPERTY I.

SI OF REPEAT II.

SI OF REPEAT III.

SI OF REPEAT IV.

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                                                                             SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS
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InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
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FRPFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASRKLPKLYGDIPPELVT 75 16

43.4%; Score 3983; DB 1; 1 Larity 46.3%; Pred. No. 1e-244; Conservative 311; Mismatches 481;

Similarity

Local

Best Loca Matches

5....

Query Match

829;

33;

Gaps

Indels 170; Length 1820;

.rsp

| : | KPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHSVFSMFI 135
 | ICTVIINCMFMANSMERSFDNDIPPEVVFIGIYILEAVIKILARGFIVDEFSFLRDPWNWL 195
: : : :: : | DFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKKLVDVMV 255
 - | IKHNCGPNPASNKDCFEKEK 300
 | DSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTQD 354 : | SWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEK 414
 : :: | MFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQA 474
 : : : : : :
EFQRAVEQLRIQQEQINDERKASLASQLTQNQEA 455 | SASDSEDDASKNPQLLEQTKRLSQNLPVDLFDEH-VD-PLHRQRALS 519 : :: | AVSILTITIQEQEKEQEPCEGKNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTELAIT 579
 | ICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVF 639
 | DSIVALLSLADVLYNTLSDNNRSFLASLRVLRYFKLAKSWPTLNTLIKIIGHSVGALGNL 699
 : : : : : : | TVVLTIVVEIFSVVGMRLFGTKFNKTAYATQERPRRRWHMDNFYHSFLVVFRILC 754
 : : : | GEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNEEKDGSLEGET 814
 | RKTKVQLALDRFRRAFSFMLHALQSFCCKKCRRKNSPRPKETTESFAGENKDSILP 870 | DARPWKEYDTDMALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPPET 930 | DSPRKKSDAVSMLSECSTIDLNDIFRN 1 | -LOKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFE 1037
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| | | | | 6 LTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASNKDC | | | 10 0 | 10 10 | | й ·· Д | | | | | | | -LOKTVSPK
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| Db 13 | Oy 76
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Db 188 | Oy 256
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Db 422 | Oy 475
Db 456 | Oy 520
Db 516 | Qy 580
Db 574 | Qy 640
Db 634 | Qy 700
Db 692 | Oy 755
Db 748 | Oy 815
Db 806 | Qy 871 | Oy 931
Db 900 | Oy 983 | 7 |

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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:

Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:

Ephydroidea: Drosophilidae: Drosophila.

NCBI_TaxID=7227:
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                                                  1004 TFIIFMILLSSGVLAFEDIYIWRRRVIKVILEYADKVFTYVFIVEMLLKWVAYGFKRYFT
                                                                                             SAWCWLDFLIVVVSVLSLMN------LPSLKSFRTLRALRPLRALSQFEGMKVVVYALI
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"Molecular analysis of the para locus, a sodium channel gene Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN).
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MEDLINE-89184571; PubMed-2538830;
Ramaswami M., Tanouye M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-1862 FROM N.A.
STRAIN-CANTON-S; TISSUE-Head;
MEDLINE-89376565; Pubmed-2550145;
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SEQUENCE OF 1-1862 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                  SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: AT LEAST THREE DIFFERENT FORMS ARE PRODUCED
BY ALTERNATIVE SPLICING OF THE PARA GENE.
DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS ($1,$2,$3,$5,$6) AND ONE POSITIVELY CHARGED
SEGMENT ($4). SEGMENTS $4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
SURLARITY: TO OTHER SODIUM CHANNEL PROTEINS.
                                       Proc. Natl. Acad. Sci. U.S.A. 86:2079-2082(1989).
-1- FUNCTION: THIS PROPEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEMBELLITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
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InterPro; IPR00636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
Pfam: PF00520; ion_trans; 4.
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NLTFVLCIIFIFAVMGMQLFGKNYHDHKDRFPDGDLPRWNFTDEMHSFMIVFRVLCG | EWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLANSFSNEEKDGSLEGETR | KTKVQLALDRFRRAFSFMLHALQSFCCKKCRRNSPKPKETT
 | SFAGENKDSILPDARPWKEYDTDMALYTGQAGAPLAPLAEVEDDVEYCGEGGA : : | TSQHSAGVQAGDLPPETKQLTSPDD | VPSEEDLHLSIQSPRKKSDAVSMLSECSTIDLN-
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DASKEDLGLDEELDEEGECEEGPLDG | HFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRP
 | VEKLLRCIDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLM: :: : | NLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVN : : | LFSGKFGRCINGTDINMYLDFTEVPNRSQCNISNYSWKVPQVNFDNVGNAYLALLQVA : : : : | 7.
1. | QKKLGGQ-DIFWTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIL: | GLIVLNMIIMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFD
 | CWVVVLSIISTLVSR-LEDSDISFPPTLFRVVRLARIGRILKLVRAARGIRTLLFALMMS | LPSLFNIGLLLELVMFIYAIFGMSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGW : | DTLLNPMLEAKEHCNSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: HEART AND UTERUS.
-1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED
SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
                                                        1647
                                                                            1707
                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 89:4893-4897(1992).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00170; NACHANNEL.
SMART; SM00015; IQ; 1.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
                                                      NTATEESEDPLGEDDFEIFYEVWEKFOPEASOFIQYSALSDFADALPEPLRVAKPNKFQF
                                                                                                                                  LVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Heart, and Fetal skeletal muscle;
MEDLINE-92279233; PubMed-1317577;
George A.L. Jr., Knittle T.J., Tamkun M.M.;
"Molecular cloning of an atypical voltage-gated sodium channel expressed in human heart and uterus: evidence for a distinct gene
                                                                                                                                                                                                                                                                                                                         TNG_HUMAN STANDARD; PRT; 1682 AA.

COLN6 HUMAN STANDARD;

COLN18;

O1-JUL-1993 (Rel. 26, Created)

T 01-JUL-1993 (Rel. 26, Last sequence update)

T 20-JUL-1993 (Rel. 26, Last semocation update)

E 20-JUL-1993 (Rel. 26, Last semocation update)

SODIUM CHANNEL PROTEIN, CARDIAC AND SKELETAL MUSCLE ALPHA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR001682; Channel_pore_Ca_Na.
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InterPro; IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
Pfam; PF00612; IQ; I.
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MIM; 182392; -.
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 :: :
 B87 MFYGGERSKHLKNGC-F | OY 1039 FIIFVILLSSGALIFEDVNI | 939 | QY 1099 AWCWLDFLIVVVSVLSLM | Qy 1157 LNVLLVCLIFWLVFCILGVN | EC01 | DD 1118 WENAKMYEDNYGNALEALLY | QY 1273 IFGSFFTLNLFIGVIIDNEN | 1178 | (A 1333 NKCQAFVFDLVTSQVFDVII | 1393 | 1298 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license gireement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS. EACH WITH 5
HYDROPHOBIC SEGMENTS ($1,52,53,55,56) AND ONE POSITIVELY CHARGED
SEGMENT ($4). SEGMENTS 54 ARE PROBABLY THE VOLTAGE-SENGORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                     1624
                                                                                                                                                                   TMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHMEKMVKLRLKDRSSSS- 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementary DNA sequence.";
Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Blochme. Brorgen MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIT FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00170; NACHANNEL. Ion transport; Voltage-gated channel;
                                                                                                                                                                                  SEIESGFLLANPFKITCEPITTIKRKQEAVSATIIQRAYKNY----RLRRNDKNTSDI
                                                                                                                          ----EHCNSSSQ--DSCQQPQIAVVYF
                        FETFGNSMLCLFQVAIFAGWDGMLDAIFNSKWSDCDPDKINPGTQVRGDCGNPSVGIFYF
                                                     VSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVWEKFDPEASQFIQYS
                                                                      ALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMK
                                                                                                                                                                                                                                                                                                                                                                                        SODIUM CHANNEL PROTEIN I, BRAIN.
Loligo bleekeri (Bleeker's squid).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
Myopsida; Loliginidae; Loligo.
NCBI_TaxID=6617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato C., Matsumoto G.; Primary structure of squid sodium channel deduced from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS
                                                                                                                                                                                                                                                                                                                                                 (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                        1522 AA
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InterPro; IPR001636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
FETFTGSMLCLFQITTSAGWDTLLNPMLEAK
                                                                                                                                                                                                                       HQVFCNGDLSS-----LDVAKVK 1761
                                                                                                                                                                                                                                         | : : |: :
HMIDGDRDVHATKEGAYFDKAKEK 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Optic lobe;
MEDLINE-92337659; PubMed=1339273;
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SEQUENCE FROM N.A.
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01-FEB-1995
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Q05973;
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CIN1_LOLBL
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307 KTFMVLN---KKRTIYRFSAKRALFILGPFNPLRSLMIRISVHSVFSMFIICTVIINCMF 145 MANSMERSFUNDIPEYVFIGIYILEAVIKILARGFIVDEFSFLRDPWNWLDFIVIGTAIA 205 CLWIFSQAGVQLFGGALRHKCVLQIHG-SPAFGKTYDEFYAEHIENSDNWLAKGNGEYVĻ 245 366 426 344 357 546 Gaps (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). TCFPGSQVN-----LSALRTFRVFRALKAISVISGLKVIVGALLRSVKKLVDVMVLTLF CLSIFALVGQQLFMGILNQKCIKHNCGPNPASNK--DCFEKE------KDSEDFIM PQLLEQTKRLSQNLPVDLFDEHVDPLHRQRALSAVSILTITIQEQEKFQEPCFPCGKNLA TLLL-QTINDKVISDITGLRTFRVLRALRTLSIIPGLKTMVNALLRALRMLISVLILILF CGTWLGSRPCPNGSTC-DKTTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRT CGNATGAGPCPTNYTCLPDIGENPNYGYTNFDSIGWSMLISFQLLTQDYWEDVYNKVIRA SCIYFVFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEKMFQEAQQLLREE KEALVAMGIDRSSLNSLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKN (POTENTIAL) (POTENTIAL) 32.1%; Score 2945; DB 1; Length 1522; 38.5%; Pred. No. 6e-179; Indels NKED (GLCNAC. . .) (POT 4CFDDB83E5436626 CRC64; %; Pred. No. 6e-179; 283; Mismatches 502; (BY HSPWTVIYFIVINFFGSLYLMNLMLAVVATAYELEVKNT---PHOSPHORYLATION REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED LINKED Phosphorylation 174113 Conservative 1022 1120 1154 1184 346 Repeat; AA; Best_Local Similarity ...Matches 650; Conserv 1124 Query Match CARBOHYD CARBOHYD CARBOHYD SEQUENCE

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                                                   SKYLVWDCSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKI
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                                                                                                                                                                                     LRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNKTA
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Tinsect calcium channels. Molecular cloning of an alpha 1-subunit from housefly (Musca domestica) muscle."; housefly (Musca domestica) muscle."; tebs Lett. 339:189-194(1994).

C. -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, C CELL MOTILITY, CELL DIVISION AND CELL DEATH (BY SIMILARITY) MDL-ALPHA INCODES A DIHYDROPYRIDINE- AND DILITAZEM-SENSITIVE CURRENT IN LARVAL BODY WALL MUSCLE.

C. -- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C. -- TISSUE SPECIFICITY: PREDOMINANTIX EXPRESSED IN THE LARVAL BODY WALL MUSCULATURE. IN ADULTS, HIGHEST EXPRESSION IN THORAX FOLLOWED BY HEAD AND AT A LOWER EXTENT BY ABDOMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                          DFEIFYEVWEKFDPEASOFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLH 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Musca.
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DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGNENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
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SERIE OF POSITIVELY CHARGED ANDINO ACIDS AT EVERY THIRD POSITION.
SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94148084; PubMed=8313972;
Grabner M., Bachmann A., Rosenthal F., Striessnig J., Schultz C.,
Tautz D., Glossmann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1).
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InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_11g.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR002048; Br-hand.
Pfam; PF00036; efhand; 1.
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Q25452;
15-JUL-1999 (
15-JUL-1999 (
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CCAM_MUSDO
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  1602
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| <pre>Ion transport; Voltage-gated channel; 1; Repeat; Multigene family;</pre> | :1on.
I: | II.
III. | IV. | CITOPLASMIC (POTENTIAL).
SI OF REPEAT I (POTENTIAL). | EXTRACELLULAR (POTENTIAL). | CYTOPLASMIC (POTENTIAL). | S3 OF REPEAT I (POTENTIAL). | S4 OF REPEAT I (POTENTIAL). | CYTOPLASMIC (POTENTIAL). | EXTRACELLULAR (POTENTIAL). | S6 OF REPEAT I (POTENTIAL). | CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL). | SELLULAR | S2 OF REPEAT II (POTENTIAL). | S3 OF REPEAT II (POTENTIAL). | EXTRACELLULAR (POTENTIAL). | S4 OF REPEAT 11 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). | S5 OF REPEAT II (POTENTIAL). | EXTRACELLULAR (POTENTIAL). | CYTOPLASMIC (POTENTIAL): | REPEAT | EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT III (POTENTIAL). | CYTOPLASMIC (POTENTIAL). | S3 OF REPEAT III (POTENTIAL).
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S5 OF REPEAT III (POTENTIAL) | SELLULAR (PO | S6 OF REPEAT III (POTENTIAL). | REPEAT | EXTRACELLULAR (POTENTIAL). | LASMIC (| REPEAT | S4 OF REPEAT IV (POTENTIAL). | LASMIC | SELLULAR | REPEAT | LEU. | ILE. | CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). | CALCIUM ION SELECTIVITY AND PERMEABILITY | (BI SIMILARIII) CALCIUM ION SELECTIVITY AND PERMEABILITY | (BY SIMILARITY).
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496 | 515 | 525 | 563
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941 | 1030 | 1055 | 1129 | 1143 | 1172 | 1191 | 1238 | 1257 | 1343 | 1362 | 570 | 1043 | 285 | 617 | 1005 | 1311 | 9901 | 1389 | 1378 | 1409 | 193874 |
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| MGILNQKCIKHNCGPNPASNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDN 332 |
| NYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVF-FFVVVIFLGSFYLLNLTL 391 |
| AUVTMAYBEQNRNVAAETBAKEK-MFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSP 450 |
| KKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTKRLSQNLPVDLFDEHVD 510 |
| PLHRQRALSAVSILTITIOEOGEKFOEPCFPCGKNLASKYLVWD 553
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| CSPQWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIGNMVFTG 613 |
| IFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDNNRSFLASLRVL 670 : : |
| RVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNKTAYATO 730
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| ERPRRWHMDNEYHSFLVVFRILGGE-WIENMWGCMQDMDGSPLCIIVFVLIMVIG 785
 : : : :
 ERPRSNFDSFYQSLLTVFQILTGEDWNVVMYDGIRAYGGVFSFGIVACIYYIILFICG 651 |
| KLVVLNLFTALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCCKKÇ 845 :: : : :::::::::: NYILLNVFLAIAVDNLADADSLSTIEKEDESQIQLD |
| RRKNSPKETTESFAGENKDSILPDARPWKEYDTDMALYTGQAGAPLAPLAEVEDDVEY 905 |
| CGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAV 965 |
| SMLSECSTIDLNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRK 102
 |
| TCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEM 108 |
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Search completed: February 27, 2002, 01:39:36 Job time: 635 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 27, 2002, 01:28:56 ; Search time 114.56 Seconds
(without alignments)
2253.585 Million cell updates/sec Run on:

1 MEERYYPVIFPDERNFRPFT.........VFCNGDLSSLDVAKVKVHND 1765 US-09-646-224A-2 9173 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*

sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_unclassified:* sp_virus:*
sp_vertebrate:* sp_organelle:* sp_rodent:* sp_plant:* sp_phage: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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44 3541.5 38.6 2031 5 | | O9YGN7 | Q9C007 | 900060 | O9WTU3 | 088420 | 088421 | 070611 | 000060 | 095788 | 060858 | Q9DF53 | Q9ER60 | Q9NYX2 | 063541 | Q9IBF1 | 028371 | 025150 | 090519 | 025439 | 094615 | 025440 | 001306 | 001307 | Q9VXF7 | 024531 | 024532 | |
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| 012829202020202020202020202020202020202020 | | 48.8 | 48.7 | 48.5 | 47.9 | 47.9 | 47.9 | 47.8 | 47.7 | 47.7 | 47.6 | 47.6 | 47.5 | | | 45.5 | 44.5 | 42.7 | 41.8 | 38.7 | 8 | 8 | æ | 38.6 | 38.6 | 38.5 | 38.5 | |
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دست | Lvs | ě. | i) | ÷. | دکت | rita. | j. | Ph. | 43 | 1. | si. | : | |

ALIGNMENTS

Rattus norvegicus (Rat). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) VOLTAGE-GATED NA CHANNEL ALPHA SUBUNIT NAN. PRT; 1765 AA PRELIMINARY; 088457 088457; RESULT Ö88457 COLORD BY NEW RESERVED TO THE POLICY RESERVED TO THE PROPERTY OF THE PROPERTY

SEQUENCE FROM N.A.
SPRAIN-SPRAGUE-DAMLEY, TISSUE-DORSAL ROOT GANGLIA;
MEDLINE-99338074; PubMed-967178;
Dib-Hajj S.D., Tyrrell L., Black J.A., Waxman S.G.;
MiaN, a novel voltage-gated Na channel, is expressed preferentially in peripheral sensory neurons and down-regulated after axotomy.";
Proc. Natl. Acad. Sci. U.S.A. 95:8963-8968(1998).

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-DORSAL ROOT GANGLIA; Tate S.N.;

SEQUENCE FROM N.A..
SEQUENCE FROM N.A..
STRAIN=SPRAGUE-DAWLEY, TISSUE-DORSAL ROOT GANGLIA;
MEDLINE-99212311; PubMed=10196578;
Tate S.N., Benn S.C., Hick C.A., John V.H.;
"Two sodium channels contribute to the TTX-R sodium current in primary EMBL; AF059030; AAC40199.1; -.
EMBL; AJ237852; CAB41850.1; -.
InterPro; IPR000636; Cation_chan_non_lig. sensory neurons."; Nat. Neurosci. 1:653-655(1998).

InterPro; IPR001682; Channel_pore_Ca_Na. InterPro; IPR001696; Na_channel. InterPro; IPR002111; Cat_channel_TrpL. Pfam; PF00520; ion_trans; 4. InterPro; IPR000734; Lipase

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            Wood P.M.,
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Pred. No. 0;
94; Mismatches
                                                         IPRO00638; Cation_chan_non_lig.
IPRO01211; Cat_channel_TrpL.
IPRO01682; Channel_pore_Ca_Na.
IPRO00734; Lipase.
IPRO01696; Na_channel.
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            A.,
      PubMed=10444332;
            L., Escayg
                                            EMBL, AF118044; AB53403.1; -. MGD; MGI:1345149; Scnlla. InterPro; IPR000636; Cation_cha
                                                                                                                                Query Match

Best Local Similarity 88.7%;
Matches 1569; Conservative 94
                                                                                        ion_trans; ... NACHANNEL
                        e, genomic
the mouse
                                         Genomics 59:309-318(1999)
            .D., Tyrrell
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PROSITE; PS00120; L.
Ionic channel.
SEQUENCE 1765 AA;
     MEDLINE=99375324;
Dib-Hajj S.D., Tyr.
Waxman S.G.;
                        "Coding sequence,
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X MEDLINE-20090627; PubMed-10623609;
XA Ggata K., Jeong S.Y., Murakami H., Hashida H., Suzuki T., Masuda N.,
RA Ggata K., Jeong S.Y., Murakami H., Hashida H., Suzuki T., Masuda N.,
RA Hirai M., Isahara K., Uchiyama Y., Goto J., Kanazawa I.;
RY "Cloning and expression study of the mouse tetrodotoxin-resistant
RT voltage-gated sodium channel alpha subunit Nar/Scnlla.";
RBL: AB031389: BA92154.1; -
DR RBL: AB031389: BA92154.1; -
DR RGD: MGI:1345149; Scnlla.
DR InterPro: IPR001682; Cation_chan_non_lig.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001682; Na_Channel.

InterPro: IPR001683; Na_Channel.

InterPro: IPR001683; Na_Channel.
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                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT NAT/SCN11A.
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88.2%; Pred. No. 0;
ive 95; Mismatches 107;
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Pfam; PF00520; ion_trans; 4.
PRINTS; PR00170; NACHANNEL.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
Ionic channel.
SEQUENCE 1765 AA; 201305 MW; FFF1D12
                                                                                                     Created)
                                                                                                 (TrEMBLrel. 15, TremBLrel. 15, TremBLrel. 17,
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                                                                                        FQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSPKKRKFFGSKTRKSFFMRGSKTAQAS
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                                                    WERLYROILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEONRNVAAETEAKEKM
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                        QIAIVYFVSYIIISLLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEIWEKFDPEA
                                         SOFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDS
                                                                              SGLDTMKTMMEEKFWEANPFKKLYEPIVTTKRKEEEQGAAVIQRAYRKHMEKMVKLRLK
                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                        Jeong S.-Y., Goto J., Hashida H., Suzuki T., Ogata K., Hirai M., Isahara K., Uchiyama Y., Kanazawa I.; "Identification of a novel human voltage-gated sodium cybubuit gene, SCN12A."; Biochem. Biophys. Res. Commun. 267:262-270(2000).
                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT SCN12A.
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InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001695; Na_channel.
InterPro; IPR002111; Cat_channel_TrpL.
Pfam: PF00520; Ion_trans; 4.
                                                                                                                          GRSSSSLQVFCNGDLSSLDVPKIKVHCD 1765
                                                                                                                  DRSSSSHQVFCNGDLSSLDVAKVKVHND 1765
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Best Local Similarity 72.9%; Pre
Matches 1316; Conservative 178;
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                                                                                                                                                                                                                                                Homo sapiens (Human).
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                                                DIIIISLIILNMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNG
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                                                                                                                                                                                                              MEERYYPVIFPDERNFRPFTSDSLAAIKKRIAIQKERKKSKDKAAAEPQPRPQLDLKASR
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                                                                                                                                                                                                                                                                                    TSAGWDTLLNPMLEAKEHCNSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Two tetrodotoxin-resistant sodium channels in human dorsal root
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UHEO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VOLTAGE-GATED SODIUM CHANNEL TYPE XI ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258;
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InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR002111; Cat_channel_TrpL.
Pfam; PF00520; ion_trans; 4
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TISSUB-DORSAL ROOT GANGLIA;
MEDLINE-20047838; Pubmed-10580103;
Dib Hajj S.D., Tyrrell L., Cummins
Waxman S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ganglion neurons.";
FEBS Lett. 462:117-120(1999).
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Best Local Similarity
Matches 1315; Conserv
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT, ALTERNATE (SCA12A-S)
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Homo sapiens (Human).
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Mammalla; Eutheria; Primates;
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Cat_channel_TrpL
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SEQUENCE FROM N.A.
STRAIN-BALBAC; TISSUE-HEART;
Zimmer T., Benndorf K.;
"The mouse heart sodium channel (mH1): cloning and characterization alternatively spliced variants.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ271477; CAB70096.1;
MGD; MGI:98251; Scn5a.
"*** FPTO; IPR000636; Cation_chan_non_lig.
"*** FPTO; IPR000636; Cation_chan_non_lig."
                                                                                                                                                                                                                                                                  DVIILGLIVLNMIIMMAESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNG
EELGILT---SVPKTLGVRHDWTWLAPLAEEEDDVEFSGEDNAQRITQPEPEQQAYELHQ
                      ETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLNDIFRNLQKTVS
                                  PKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSS
                                                                                                               GALIFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIV
                                                                                                                             VVSVLSLMNLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPAILNVLLVCLIFWL
                                                                                                                                                                                                         VFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQCNISNYSWKVPQVNFDNVGNAYL
                                                                                                                                                                                                                                                      ALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVII
                                                                                                                                                                                                                                                                                                    DNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLGTKKPQKPIPRPLNKCQAFVFDLVTSQVF
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Sciurognathi; Muridae; Murinae; Mus
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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InterPro: IPR00111; Cat_channel_TrpL.
InterPro: IPR001182; Channel_pore_Ca_Na.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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Ionic channel,
SEQUENCE 2019 AA;
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                                                                                        VFSMFIICTVIINCMFMANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD 183
                                                                                                                             EFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGAL 243
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                                                 ADDENSTAGESESHRTSLLVPWPLRRPSTQGQPGFGTSAPGHVLNGKRNSTVDCNGVVSL
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                                                                                                                                                                                                                                                                           AMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNV
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LTITMCIVLNTLFMALEHYNMTAEFEEMLQVGNLVFTGIFTAEMFKIIALDPYYYFQQG
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                                      NFRPFTSDSLAAIKKRIAIQKER-----KKSKDKAAAEPQPRPQLDLKASRKLPKLYGDI
                    262;
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  Length
                    Indels
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Query Match 51.6%; Score 4730; DB 11;
Best Local Similarity 50.1%; Pred. No. 0;
Matches 976; Conservative 286; Mismatches 423;
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175 411 471 178 235 231 292 291 349 351 409 446 EDNKSPRSDPYNQRRMSFLGLASGKRRASHGSVFHFRSPGRDISLPEGVTDDGVFPGDHE 531 KTRKSFFMRG-----SKTAQASASDS---EDDASKNPQLLEQTKRLSQN-LPVDL 504 Gaps LPKLYGDIPPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSL 121 62 61 YPVIFPDERNFRPFTSDSLAAIKKRIA----IQKERKKSKDKAAAEPQPRPQLDLKASRK FPIGSLETNNFRRFTPESLVEIEKQIAAKQGTKKAREKHREQKDQEEKPRPQLDLKACNQ MIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIP---EYVFIGIYILEAVIKILAR 123 AIKVSVHSWFSLFITVTILVNCVCMTRT-----DLPEKIEYVFTVIYTFEALIKILAR GFIVDEFSFLRDPWNWLDFIVIGTAIATCFPGSQVNL---SALRTFRVFRALKAISVISG ---KDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFR human LKVIVGALLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASN---VMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAET Euteleostom1; S.L.; ij 241; Length 1956 ŝ SEQUENCE FROM N.A.
TISSUB-DORSAL ROOF GANGLIA;
MEDLINE-DORSAL ROOF GANGLIA;
MEDLINE-S. F. Vooh B.D., Inikoka M., Obernolte R.A., Naylor S.
Herman R.C., Eglen R.M., Hunter J.C., Sangameswaran L.;
"A tetrodotoxin-resistant voltage-gated sodium channel from I dorsal root ganglia, hPN3/SCN10A.";
Pain 78:107-114(1998). Naylor L.; Homo sapiens (Human). Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Indels Rabert D.K., Koch B.D., Ilnicka M., Obernolte R.A., Nayl Herman R.C., Eglen R.M., Hunter J.C., Sangameswaran L.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AFI17907; AAD30863.1; -. InterPro; IPR000636; Cation_chan_non_lig. InterPro; IPR001682; Channel_pore_Ca_Na. InterPro; IPR001695; Na_channel. InterPro; IPR002111; Cat_channel. InterPro; IPR002111; Cat_channel_TrpL. Pf00520; ion_trans; 4. F24B73E7C211DA5E CRC64; 429; EAKEKMFQEAQQLLREEKEALVAMGIDRSSLNSLQAS----DB 11 Similarity 51.1%; Pred. No. 0; 978; Conservative 266; Mismatches ----SPKKRKFFGS----SF----SPKKRKFFGS-----4669.5; 50.9%; Score 51.1%; Pred. 1956 AA; 220563 MW; SEQUENCE FROM N.A. TISSUE-DORSAL ROOT GANGLIA; PRINTS; PR00170; NACHANNEL

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| (y) 1502 KKGSGIDDIFNFETFTGSMLCLFQITTSAGNDTLLNPMLE-AKEHCNSSSQDSC 1554 (i) ::! : : : | RESULT 9 P70276 ID P70276 P70276 TO 1-FEB-1997 (TrEMBLrel. 02, Created) FT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) FT 01-FEB-1997 (TrEMBLrel. 17, Last annotation update) FT 01-TEB-1997 (TrEMBLrel. 17, Last annotation update) FT 01-MNNEL. FT 01-MNNEL. FT 01-EB-1997 (TrEMBLrel. 17, Last annotation update) FT 01-MNNEL. FT 01-MNNEL. FT 01-MNNEL. FT 02-MNNEL. FT 03-MNS NNS NNS NNS NNS NNS NNS NNS NNS NNS | RP SEQUENCE FROM N.A. SCOURS OF TAIN 129/SV; AM MEDIJNE-97288517; PubMed-9143495; AM SOUSIOVA V., FOX M., Wood J.N., Akopian A.N.; RT "Cloning and characterization of a mouse sensory neuron tetrodotoxingram of the characterization of a mouse sensory neuron tetrodotoxingram of the characterization of a mouse sensory neuron tetrodotoxingram of the characterization of a mouse sensory neuron tetrodotoxingram of the characterization of a mouse sensory neuron tetrodotoxingram of the characterization of a mouse sensory neuron tetrodotoxingram of the characterization of a mouse sensory neuron tetrodotoxingram of a mouse sensory neuron of a mouse sensory neuron of a mouse sensory neuron of a mouse sensory neu | Ouery Match 89.7%; Score 4555; DB 11; Length 1958; Best Local Similarity 50.4%; Pred. No. 0; Matches 956; Conservative 273; Mismatches 444; Indels 224; Gaps 3. 4y 15 NFRPFTSDSLAAIKKRIAIOKERKKSKDKAAAEPOPRPQLDLKASRKLPKLYGDIP 70 11 |
|--|---|--|---|
| Db 532 SHRGSLLLGGGAGQQFLPRSPLPQPSNPDSRHGEDEHQPPPTSELAPGAVDVSA 586 Qy 505 FDEHVD-PLHRQRALSAVSILTITIQEQEKFQEPCFPGGRNLASKYLVWD 553 | Qy 732 RPRREWHMDNEYHSELVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLN 791 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | OY 922 QAGDLPPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRKKSDAVSMLSECSTIDLND 978 1 | OY 1207 NISNYSWKVPQVNEDNVCNAYLALLQVATYKGWLEIMNAAVDSREKDEQDEFEANL 1262 1333 KIQNSTGSFFWVNYKVNFDNVAMGYLALLQVATYKGWLEIMNAAVDSREKDEQDEFEANL 1262 1345 KIQNSTGSFFWVNYKVNFDNVAMGYLALLQVATFKGWMDIMYAAVDSREVNMQPKWEDNV 1392 155 YAYLYFVYFIIFGSFFTLNLFIGVIIDNFNQOQKKLGGQDIFMTEEQKKYYNAMKKLGTK 1322 156 YAYLYFVYFIIFGGFFTLNLFYGVIIDNFNQOQKKLGGODIFMTEEQKKYYNAMKKLGTK 1322 157 YMYLYFYIFIIFGGFFTLNLFYGVIIDNFNQOKKLGGODIFMTEEQKKYYNAMKKLGSK 1452 158 YMYLYFYIFIIFGGFFTLNLFYGVIIDNFNQOKKLGGODIFMTEEQKKYYNAMKKLGSK 1452 158 YMYLYFYIFIIFGGFFTLNLFYGVIIDNFNQOKKLGGODIFMTEEQKKYYNAMKKLGSK 1452 158 APQKPIPRPLNKFQGFVFDIYTRQAFDITIMVLICLNMITMMVETDDQSEEKTKILGKIN 1512 159 KPQKPIPRPLNKFQGFVFDIYTRQAFDITIMVLICLNMITMMVETDDQSEEKTKILGKIN 1512 150 THIS SPOKPIPRELIKFARARGYYFTNGWNVFDFIVVVLSIASLIFSALLKSLOSYFSPTLF 1572 150 THIS SPOKPIPRELIKLRAARGIKTLLFALMMSLPSLFNIGLLFLYWFIXAIFGMSWFSKV 1501 1513 QFFVAVFTGECVMKMFALRQYYFTLFALMMSLPSLFNIGLLFLYWFIXAIFGMSSFPHV 1632 |

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241 HSVRKI | KKLVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPASNKDCFEK
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301 -PGTTD | PIMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVMTODSWER :: : : : : : | 358
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Dp | 359 LYROII
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360 LYQQTI | OILRTSGIYEVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEKMFOE
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720 PYYYFC | FRHGMNVFDSIVALLSLADVLYNTLSDNNRSFLASLRVLRVFKLAKSWPTLNTLIK | 687 |
| Qy | B IIGH | VEIFSVVGMRLFGTKFNKTAYATQERPRRRWHMDNFYH | 4 |
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| Ογ | 46 FLVVF | RILCGEWIENMWGCMQDMDGSPLCIIVFVLIMVIGKLVVLNLFIALLLNSFSNE- | |
| q | 8 FLVVF | ILCGEWIENMWVCM-EVSONYICLTLFLTVMVLGNLVVLNLFIALLENSFSADI | 968 |
| οy | 5 E | WQLALDRFRRAFSFMLHALQSFCCKKCRRK- | 848 |
| QQ | rape | SEVNNLQLALARIQVLGHRASRAITSYIRSHCF | 950 |
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| qq | 1056 EDLAPYLGE | : :1 : | 1111 |
| ογ | 993 PDRCFPK | :
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| q | 1112 PDDCF7 | GCTRRCPCCKVNTSKSPWATGWQVRKTCYRIVEHSWFESFIIFMILLS | 1171 |
| Oy
Dp | 1053 FEDVNLPS

 172 FEDNYLES | LPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSV | 1112 |
| δy | 13 [| NLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAII | 116 |
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                         FWLVFCILGVNLFSGKFGRCINGTDINMY - - LDFTEVPNRSQC - - - - NISNYSWKVPQVN 1219
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PubMed=8663093;
Sangamean L.B., Delgado S.G., Fish L.M., Koch B.D., Jakeman L.B.,
Stongamean and L.B., Delgado S.G., Eglen R.M., Herman R.C.;
Stewart G.R., Sze P., Hunter J.C., Eglen R.M., Herman R.C.;
J. Biol. Chem. 271:13292-13292(1996).
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062968;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SODIUM CHANNEL PN3.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Solurognathi; Murinae; Rattus.
NCBI_TaxID-10116;
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MEDLINE=96198040; PubMed=8626372;
Sangameswaran L., Delgado S.G., Fish L.M., Koch B.D., Jakeman L.B.,
Stewart G.R., Sze P., Hunter J.C., Eglen R.M., Herman R.C.;
"Structure and function of a novel voltage-gated, tetrodotoxin-
resistant sodium channel specific to sensory neurons.";
J. Biol. Chem. 271:5953-597(1996).
EMBL, U53833: AAC52619.1;
                                                                                                                                                                                                                                                                          LRQHYFTNGWNLFDCVVVVLSIISTLVSR-LEDSDISFPPTLFRVVRLARIGRILRLVRA
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InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IRP00111; Cat_channel_TrpL.
Pfam; PF00555; ion_trans; 4.
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                                                      Length 1956;
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                               8FC58EDAD263AC67 CRC64;
                                                    Query Match 49.6%; Score 4553; DB 11;
Best Local Similarity 51.1%; Pred. No. 0;
Matches 966; Conservative 269; Mismatches 446;
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      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       TISSUE-THYROID;
MEDLINE=95237189; PubMed=7720699;
Klugbauer N., Lacinova L., Flockerzi V., Hofmann F.;
Klugbauer N., Lacinova L., Flockerzi V., Hofmann F.;
Structure and functional expression of a new member of tetrodotoxin-sensitive voltage-activated sodium channel human neuroendocrine cells.";
EMBO J. 14:1084-1090(1995).
                                                                                                                                                                                                     1977 AA; 225195 MW; 17D67CBC32BC15FB CRC64;
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InterPro; IPR000048; IQ.
InterPro; IPR0000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR001595; Na_channel_rrpL.
Pfan; PF00520; Ion_trans; 4.
Pfan; PF00612; IQ; I.
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49.5%; Pred. No. 0;
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SMART; SM00015; IQ;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Nature 379:257-262(1955).
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Interpro: IPR001686; Na_channel.
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WVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSD-NNRSFLASL, 667 1984 Ionic channel. NON_TER 198 SEQUENCE 198 SASD----Query Match Machine West Control of the Control 1461 CLFQITTSAGWDTLLNPMLE-AKEHC-----NSSSQDSCQQPQIAVVYFVSYIIISFLI 1574 1715 VVNMYIAVILENFNVATEESTEPLSEDDFDMFYETWEKFDPEATQFIAFSALSDFADTLS 1774 SEQUENCE FROM N.A.
MEDLINE-97188502; PubMed-9037087;
Toledo-Aral J.J., Moss B.L., He Z.J., Koszowski A.G., Whisenand T.,
Levinson S.R., Wolf J.J., Silos-Santiago I., Halegoua S., Mandel G.;
"Identification of PMI, a predominant voltage-dependent sodium channel expressed principally in peripheral neurons.",
Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997). EPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEA 1694 ы Н Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus. SEQUENCE FROM N.A.
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STANGAMESWATAN L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
Ilnicka M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzoumaka J.
Stewart G.R., Herman R.C., Chan H., Egien R.M., Hunter J.C.;
EMBL; U79568; AAB50403.1;
EMBL; U79568; AAB50403.1;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Rattus norvegicus (Rat). "Genetic mapping of the peripheral sodium channel ScnlOa, in the mouse."; NPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHM 1728 Z PRT; 1984 {2]
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126 490 548 424 484 Gaps ----SEDFINGGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNFGWSFLAMFRVWTQDSWE ARRSSRTSLFSFKGRGRDLGSETBFADDEHSIFGDNESRRGSLFVPHRPRERRSSNISQA EQTKRLSQN - - LPVDLFDEHVDPLHRQRALSAVSILTITIQEQEKFQEPCFPCGKNLASK PPELVTKPLEDLDPYYKDHKTFWLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS VFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIGIYILEAVIKILARGFIVDEFSFLR DPWNWLDFIVIGTAIATCFPGSQVNLSALRTFRVFRALKAISVISGLKVIVGALLRSVKK 305 YLEGSKDALLCGFSTDSGQCPEGYICVKAGRNPDYGYTSFDTFSWAFLALFRLMTQDYWE **OKMSSGEEKGDDEKLSKSGSEESIRKKSFHLGVEGHHRTREKRLSTPNQSPLSIRGSLFS** ---RKSFFM-----RGSKTAQA -----SEDDASKNPQLL SRSPPVLPVNGKMHSAVDCNGVVSLVDGPSALMLPNGQLLPEVIIDKATSDDSGTTNQM-PDERNFRPFTSDSLAAIKKRIAIQKERK-KSKDKAAAEPQPRPQLDLKASRKLPKLYGDI LVDVMVLTLFCLSIFALVGQQLFMGILNQKCIKHNCGPNPA-.SNKDCFEKEKD-.... RLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEEQNRNVAAETEAKEKMFQ EAQQLLR---EEKEALVA-------MGIDRSSLNSLQASSFSPKKR-----DB 11; Length 1984; 386C38B9B5097091 CRC64; "...erPro; IPR001682; Cation_chan_non_lig.
R InterPro; IPR001682; Channel_pore_Ca_Na.
R InterPro; IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
Pfam; PF00612; IO; 1.
PMINTS; PR00170.... 49.5%; Score 4541.5; 48.9%; Pred. No. 0; 291; Mismatches -----KFFGSKT----226037 MW; PRINTS; PR00170; NACHANNEL SMART; SM00015; IQ; 1. Conservative 1984 1984 AA; Local Similarity nes 954; Conserv

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453 544 474 604

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| A 726
C 896 | ik 786
N 955 | R 846
S 1014 | E 904
N 1050 | Q 956
D 1110 | R 1013
D 1169 | N 1073
K 1229 | T 1126
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 | II 1361
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E 1766 | L 1652
 | E 1712
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| RVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKFNK-TA
 : | YATQERPRRRWHMDNFYHSFLVVFRILCGEWIENNWGCMQDMDGSPLCIIVFVLIMVIGK : : : : | LVVLNLFIALLLNSFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHALQSFCCKKCR | RKNSPKPTESFAGENKDSILPDARPWKEYDTDMALYTGQAGAPLAPLAEVEDDVE : | YCGEGGALPTSQHSAGVQAGDLPPETKQLTSPDDQG-VEMEVFSEEDLHLSIQ
: | SP-RKKSDAVSMLSECSTIDLNDIFRNLQKTVSPKRQPDRCFPRGLSCHFLCHKTDKR | KSPWVLWWNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDN : | IFTFIFLLEMILKWVAFGFRRYFTSAWCWLDFLIVVVSVLSLMNLPSLKSFRT
 : : : : : : : : | LRALRPLRALSGFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCI
 | NGTDINMYLDFTEVPNRSQCNIS-NYSWKVPQVNFDNVGNAYLALLQVATYKGWLE
 : :: : | IMNAAVDSREKDEQPDFEANLYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQOKKLGGQ
 | DIEMTEEOKKYYNAMKKLGTKKPOKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMI
 | IMMAESADQPKDVKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGMNLFDCVVVVLSI
 | IST-LVSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLENIG : | LLLFLVWFIYAIFGMSWFSKVKKGSGIDDIFNFETFGSMLCLFQITTSAGWDTLLNPML | EAKEHCNSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATE: | ESEDPLGEDDFEIFYEWWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVWDL
 : | PMVMGBRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEBKFMEANPFKKLYEPIVTTTKRKE
 |
| 668 | 727 | 787 | 847
1015 | 905 | 957 | 1014 | 1074 | 1127 | 1187 | 1242 | 1302 | 1362 | 1422 | 1481 | 1541 | 1593
1767 | 1653
1827 |
| Qy
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Db | Qy |

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Chen J., Ikeda S.R., Lang W., Isales C.M., Wei X.;

"Molecular cloning of a putative tetrodotoxin-resistant sodium channel
from dog nodose ganglion neurons.";

Gene 202:7-14(1997).

EMBL: U60590; AAC39164.1;

EMBL: U60590; AAC39164.1;

InterPro: IPR001683; Cation_Loan_non_lig.

InterPro: IPR001685; Cation_Loan_non_lig.

InterPro: IPR001696; Na_channel.

InterPro: IPR002111; Cat_channel_TrpL.

Fiam: PF00220; ion_trans; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 FEKEK----DSEDF----IMCGTWLGSRPCPNGSTCDKTTLNPDNNYTKFDNF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 GWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLAVVTMAYEE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 FP----DERNFRPFTSDSLAAIKKRIAIQKERKKSKDK----AAAEPQPRPQLDLKASRK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GFIVDEFSFLRDPWNWLDFIVIGTAI---ATCFPGSQVNLSALRTFRVFRALKAISVISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Olordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
49.4%; Score 4532; DB 6; Length 1962;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 960; Conservative 280; Mismatches 437; Indels 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1962 AA; 220700 MW; 5D32D20D4AF47A68 CRC64;
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                                                                                              046669 PRELIMINARY; PRT; 1962 AA. 04669; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TTX-RESISTANT SODIUM CHANNEL.
1713 EEQGAAVIQRAYRK-----HMEKMVKLRLKD 1738
               || | | :|||||||
1887 EEVSATIIQRAYRRYRLRQHVKNISSIYIKD 1917
                                                                                                                                                                                                                                                                                            MEDLINE-98087411; PubMed-9427539;
                                                                                                                                                                                        Canis familiaris (Dog)
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SEQUENCE FROM N.A.
STRAIN-MONGREL;
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824 | 782
883 | 837
937 | 880
994 | 935 | 982 | 1042 | 1102 | 1155 | 1210 | 1266 | 1326 | 1386 | 1442 |
| : :: KPRVSEGSTDDNKSPQSDPYNQRRMSFLGLTSGRRRASHGSVFHFRTPCLDTSFPDGVTD | | SQ-NLPVDLFDEHV-DPLHRQRALSAVSILTITIQEQEKFQEPCFPCGKN : | LASKYLVWDCSPOWLCIKKVLRTIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTIL | KIGNWVFTGIFIAEMCLKIIALDPYHYFRHGWNVFDSIVALLSLADVLYNTLSDNNRSFL
 | ASLRVLRVFKLAKSWPTLNTLIKIIGHSVGALGNLTVVLTIVVFIFSVVGMRLFGTKF: | NKTAYATQERPRRRWHMDNFYHSFLVVFRILCGEWIENMWGCMQDMDGSPLCIIVFVLIM : | VIGKLVVLNLFIALLLASFSNEEKDGSLEGETRKTKVQLALDRFRRAFSFMLHAL
 | QSFCCKKCRRKNSPKPTTESFAGENKDSILPDARPWKEYDT : | DMALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGD-LPPET-KQLTS | PDDQGVEMEVFSEEDLALSIQSPRKKSDAVSMLSECSTIDLNDIFRN | LQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQIVKHSWFESFIIF : : | VILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWVAFGFRRYFTSAWCW: | LDFLIVVVSVLSLMNLPSLKSFRTLRALRPLRALSQFEGMKVVVYALISAIPA | ILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSQCNISN : | YSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANLYAYL
:: | YEVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFWTEEQKKYYNAMKKLGTKKPQK
 : | PIPRPLNKCQAFVPDLVTSQVFDVIILGLIVLNMINMAESADQPKDVKKTFDILNIAFV | VIPTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISFPPTLFR |
| 472 | 458 | 497 | 545 | 605 | 665 | 723 | 783 | 838
938 | 881
995 | 936 | 983 | 1043 | 1103 | 1156 | 1211 | 1267 | 1327 | 1387 |
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o | Oy
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Op | O.y | ογ |

1503 KGSGIDDIENFETFTGSMLCLFQITTSAGWDTLLNPMLE-AKEHC----NSSSQDSCQ 1555 1616 EASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFAFTTRVLG 1675 1524 AVFTGECVMKMFALRHYYFTNGWNVFDFIVVVLSIGSLVFSVILTSLEN---YFSPTUFR 1580 PPELVTKPLEDLDPYYKDHKTFMVLNKKRTIYRFSAKRALFILGPFNPLRSLMIRISVHS 129 11 PDERNFRPFTSDSLAAIKKRIAIQKERK-KSKDKAAAEPQPRPQLDLKASRKLPKLYGDI 69 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN -2001 (TrEMBLrel. 17, Last annotation update)
SODIUM CHANNEL ALPHA-SUBENIT.
SODIUM CHANNEL ALPHA-SUBENIT.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus. SEQUENCE FROM N.A.
STRAIN=NEW ZEALAND WHITE; TISSUE=SCIATIC NERVE;
MEDILINE=96074641; Pubmed=1479931;
Belcher S.M., Zerillo C.A., Levenson R., Ritchie J.M., Howe J.R.;
"Cloning of a sodium channel alpha subunit from rabbit Schwann cells."; DSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRKHM 1728 Length 1984; 1984 AA; 225748 MW; 98F76860C9866AA0 CRC64; Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).

EMBL, U35238; AAA89159.1; -.

InterPro; IPR000048; IQ.

InterPro; IPR0000636; Cation_chan_non_lig.

InterPro; IPR001682; Channel_pore_Ca_Na.

InterPro; IPR001596; Na_channel.

InterPro; IPR002111; Cat_channel_TrpL.

Pfam; PF00520; Ion_trans; 4.

Pfam; PF00520; IO. 1. ry Match 49.2%; Score 4515; DB 6; t Local Similarity 48.7%; Pred. No. 7e-318; ches 948; Conservative 286; Mismatches 458; PRT; 1984 AA PRINTS; PR00170; NACHANNEL SMART; SM00015; IQ; 1. PRELIMINARY; Ionic channel 028644 028644; 1676 20 49 130 127

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1485 DRLHCMDVLFAFTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKRKEEEQGA 1717 ESADQPKDVKKTFDILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTL INMYLDFTEVPNRSQC-----NISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNA VSRLEDSDISFPPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFL RPLRALSQFEGMKVVVYALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTD TEEQKKYYNAMKKLGTKKPQKP1PRPLNKCQAFVFDLVTSQVFDV11LGLIVLNM11MMA ----KEHCNSSSQDSCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDP AVIQRAYRKHMEKMVKLRLKDRSSSS 1743

01:38:16 completed: February 27, 2002, e: 560 sec

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| Result Query Ouery DB ID Description | 299 100.0 299 6 AX017219
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6 160.4 53.6 5334 6 E36125
7 160 53.5 5905 10 AF059030 | 8 159.2 53.2 5858 10 AFI18044 | 159.2 53.2 5321 10 ABOS1509
158.4 53.0 5897 6 AXO17217 | 45.8 15.3 5874 9 AF117907 | 13 44.2 14.8 6726 4 CFU60590
14 38.6 12.9 128398 9 AC004817 | 38.4 12.8 652/ 6 A58859 | 1/ 3/.8 12.6 6344 10 KNU53833
18 37.6 12.6 167372 9 AC004945 | 19 36.6 12.2 149490 2 AL589985 | c 23 36.2 12.1 19534 2 AC0U9451 AC0U9451 Homo sapt
c 23 36.2 12.1 199534 2 AC025959 AC025959 Homo sapt
c 24 36 12.0 116106 9 AL136080 AL136080 Human DNA
25 36 12.0 145105 2 AC018432 AC018432 Homo sapt | 36 12.0 172052 9 ALI57769
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31 35.6 11.9 129473 2 AC040158 | 35.6 11.9 143900 2 AC092137 AC092137 Homo 35.4 11.8 39854 9 AC020954 AC020954 Homo | 35.4 11.8 110000 2 AC008576_0 AC008576 Homo s 35.4 11.8 110000 2 AC079517_3 Continuation (4 | 36 35.4 11.8 157921 2 AC027726 AC08760 AC008760 Homo s | 38 34.8 11.6 6373 10 MMSNS
39 34.6 11.6 205195 2 AC025963 | 40 34.4 11.5 163067 2 AC022959 AC022959 Homo sa
41 34.4 11.5 211357 2 AC021136 AC021136 Homo sa | 42 34.2 11.4 6822 10 RNSCIII Y00766 Rat mF
43 34.2 11.4 141534 9 CNS01DS0 AL121603 Humar | c 44 34.2 11.4 186118 2
45 33.8 11.3 68692 9 | . ALIGNMENTS | . KESULT 1 | NO | AX017219
AX017219.1 | KEYWORDS SOURCE human. | Euk
Man | REFERENCE 1 (bases 1 to 299) AUTHORS Tate,S.N., Grose,D.T. and Hick,C.A. | TITLE Man COURNAL Pat TAT |) in ((ap) | SOCIECT ACCEPTANT CARD MONOR |
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| GenCore version 4.5 | copyrignt (c) 1993 - 2000 | OM nucleic - nucleic search, using sw model | Run on: February 26, 2002, 22:39:07; Search time 8647.11 Seconds (without alignments) 570.440 Million cell updates/sec | | Seriect score: 299 Seried Sequence: 1 atcctadadacadactiti | | Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0 | Searched: 1472140 seqs, 8248589755 residues | Total number of hits satisfying chosen parameters: 2944280 | Minimum DB seq length: 0 Maximum DB seq length: 2000000000 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | Database : GenEmb]:* | 1:
2: | | | | | | | | | 21: em_ov:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 5728) Jeong, S.Y., Goto,J., Hashida,H., Suzuki,T., Ogata,K., Masuda,N., Hiral,M., Isahara,K., Uchiyama,Y. and Kanazawa,I. Identification of a novel human voltage-gated sodium channel alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jeong,S.-Y., Suzuki,T., Hashida,H., Ogata,K., Masuda,M., Goto,J.
and Kanazawa,I.
                                                                                                                                                                                                                                                                                Direct Submission
Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,
Tokyo University, 7-3-1 Hongo, Bukyo-ku, Tokyo 113-8655, Japan
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                                                                  Length 299;
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/db_xref="taxon:9606"
/chromosome="3"
//map="3p21.3-p23"
/db_xref="taxon:9606"
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200. .4534
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/gene="SCN12A"
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                                                               Ouery Match 100.
Best Local Similarity 100.
Matches 299; Conservative
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HEDBHODPLODRALSAVSLITITHMKRQEKSOFECLPGGBANGSKYLWWGCPQMLCV
KRVLRTWMTDPFTELATICII INTVFLAMBHKMBASFEKMINGINLVFTSFTARM
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAM
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                                         PDYNYTNFDNFGWSELAMFRLMTQDSWEKLYQQTLRTTGLYSVEFIVVIFLGSFYLI
NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQQLLKEEKEALVAMGIDRSSLTSLET
                                                                                                                                                                                                                                                                                                                                                                                                 GKCINGTDSVINYTITNKSQCESGNESWINQKVNFDNVGNAYLALLQVATFKGWDDI
TAAAUDSTEREQQDEFESBNSLGYIYEVVBIFGSEFTLALEIGVIIDNFNQQQKKILGG
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NMISWMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGWLFDCVY
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1 (bass: Eutheria; Primates; Catarrhini; Hominidae; Homo.
Jeong, S. Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I.
Identification of a novel human voltage-gated sodium channel alpha Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)

2 (bases: 1 to 6528)
Jeong, S. Y., Suzuki, T., Hashida, H., Masuda, N., Goto, J. and
                     GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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Homo sapiens voltage-gated sodium channel alpha subunit SCN12A
(SCN12A) mRNA, complete cds.
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Pred. No. 4e-74;
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97.78;
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Best Local Similarity
Matches 291; Conserv
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GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQOTLRTTGLYSVFFIVVIFLGSFYLI
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KKVLRTVMTDPFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WCRKQNLPQQKEVAGGCAAQSKDIIPLYMEMRRGSETQEELGILTSVPKTLGVRHDWT
WLAPLAEEEDDVEFSGEDNAARITQPEPEQQAYELHQENKK7TSQRVQSVEIDMFSED
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LLNCTDIIFTHFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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SWPTLAKTIKIGNSVGALGNIFVVLVIVIFFERSVGAMCLFGRSFROKSFRLCNPTG
SPTSCLRHWHKDPFRFELVPRILCGEWIENWRCMOBANASSLCV 1VFILITY1G
KLVVLNLFIALLLNSFSNEERNGNLEGBARKTKVOLALDRFRRAFCFVRHTLEHFCHK
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GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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ODSTFWTEGRYKYYNAMKKLGSKKPQRPPPRENKCQGLVFDIVTSQIFDIIISLILIL
NMISNMAESYNQPKAMKKLLCHLIMWYPVPTTLECLIKIFALRQYYFTNGWNLFDCVI
VLESIVSTMISTLEDROWEIPPPPTLFRKIVRLARIGRILARVARARGIRTLLFALMMSL
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WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENFNTA
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VMDLPMVSEDRLHCMDIILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
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                                                       School of Medicine,
okyo 113-0033, Japan
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                        Direct Submission
Submitted (27-NOV-1998) Neurology, Graduate School of Mec
Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033
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Pred. No. 4e-74;
0; Mismatches 6;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                           /tissue_type="brain"
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                /chromosome="3'
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200. 5575
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Kanazawa,I.
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BUYNTWAYTENGYBEKLAYODSWELLYQOTLRTFGLYSVEFFIYUYTENGYFLISPLII
NLTLAYVTMAYTEQRINNYAAETEAKERMFQDEAQOLLKEEKEALVAMGIDENSSITSLET
SYFTPKKRRKLFGNKRRKSFFLRESGKDQPPGSDSDEDCQKKPOLLEGOTKRLSQNLSLD
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GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFMVLNRKRTIYR
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GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens voltage-gated sodium channel type XI alpha subunit (SCN11A) mRNA, complete cds.
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Dib-Haji,S.D., Tyrrell,L., Cummins,T.R., Black,J.A., Wood,P.M. Waxman,S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Two tetrodotoxin-resistant sodium channels in human dorsal root
/product="voltage-gated sodium channel type XI alpha
                                                                                                                            subunit; TTX-R sodium channel"
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/db_xref="taxon:9606"
/chromosome="3"
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/db_xref="G1:6572950"
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/gene="SCN11A"
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MMISMALESYNOPRAMKSILDHLNWYPVYIFTLECLIKIFPALRQYYFTNGWILFDCVV
VLLSTATISTLENOGHIPPPPTLFRIVRLARIGCHIKTRARARGIRTLLFALMMSL
PSLFNIGLLELMINTYAILGMNWFSKVNPESGIDDIFNFKTFASRUCLFQISTSA
WDSLLSPMIRSKESONSSSRNCHLPGIATSYFVSYIIISFLIVWNYIAVILENFWTA
VMDLPWYSEDRLHCMUNILFAFTRAYLGGSDGCLDSWRAMMERKFWEANRYRYGFL
VMDLPWYSEDRLHCMUNILFAFTRYFUGGSGGLDSWRAMMERKFWEANPA
TTKRKEEERGAAIIQKAFRKYMMKVTKGDGGDQUDLENGPHSPLQTIKCTFPIYY
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C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12N15/02,C12P21/02, PC
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(C12P21/02,C12R1:91),(C12P21/08,C12R1:91),C12N15/00,C12N5/00,
C12N15/00,
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20-NOV-1997 US 60/066225
PAUL SHATUA DAITORICHI,LINDA MARIE FISH,RINA KEIRU,
AS KENES RAMBERT,
                                                                                                                                                                                                                                                                                                                                                                                        1;
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Sciurognathi; Muridae;
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nerve tissue.
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Paul, S.D.L.L., Fish, R.K.D.D., Rambert and Laksmi, S. Nucleic acid encoding sodium channel of nerve tissue Patent: JP 1999235186-A 1 31-AUG-1999;
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Pred. No. 5.4e-52;
0; Mismatches 6;
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/rpt_family="Alu-Sc"
/rpt_type=dispersed
6165. 6170
/gene="SCN11A"
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Mammalia; Eutheria; Rodentia;
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/gene="SCN11A"
5689. FOF:
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JP 1999235186-A/1
31-AUG-1999
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96.9%;
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                                                                                                                                                                                                                                                                 113 agatgagcggaatttccgcccttcacttccgactcttggctgcaattgagaagcggat 172
                                                                                                                                                                                                                                                                                                                      tgocatccaaaaggagaaaaagaagtctaaagaccagacaggagaagtacccagcctca 232
                                                                                                                                                                                                                                                                                                                                                                                         171 TGCTATCCAAAAGGAGGAGGAAGAAGTCCCAAAGACAAGGCGGCAGCTGAGCCCCAGCCTCG 230
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1997 US 60/066225
PAUL SHATUA DAITORICHI,LINDA MARIE FISH,RINA KEIRU,
                                                                                                                                                                                                                     1;
                                                                                                                                                                                       Length 5908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 07-
nerve tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 5334)
Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.
Nucleic acid encoding sodium channel of nerve tissue
Patent: JP 1999235186-A 4 31-AUG-1999;
F HOFFMANN LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ce 1. .5334 / /organism='Artificial Sequence'
Location/Qualifiers
                                                                                                                                                                                                                    Indels
                                                         (rat)'

    .5908
    /organism='Rattus sp.

                                                                                                                                                                                                                    42;
                                                                                                                                                                                         DB 6;
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E36125 5334 bp DNA
Mocleic acid encoding sodium channel of
E36125
E36125.1 GI:13022508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                       56.1%; Score 167.8; DB (82.6%; Pred. No. 9.7e-41; ive 0; Mismatches 43
                                                                                                                              1525
                                                                                                 /organism="Rattus sp."
/db_xref="taxon:10118"
| 1474 c 1451 g 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-1999
20-NOV-1998 JP 1998331769
20-NOV-1997 US 60/0662
                                                                        Location/Qualifiers
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JP 1999235186-A/4
(C12N5/00,C12R1:91)
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                                                                                     .5908
                                                                                                                                                                                                     al Similarity 82.6
204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP 1999235186-A/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified
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unclassified
                                             source
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BASE COUNT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
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AF118044
LOCUS
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KEYWORDS
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YVFIGIYILEAVIKILARGFIVDEFSFLRDFWNWLDFIVIGTAIATCFPGSGVNLSAL
RFFVFRALKAISVISGLKVSVKKLVDVWVLTLFCLSIFALVGQQLFMGIL
NOKCIKHNGCPNPSATROTEEEFINGGTWLGSRPCPNGSTCDKTTLNPDNN
TKFDNFGWSFLAMFRVWTQDSWERLYRQILKTSGIYFVFFFVVVIFLGSFYLLNLTLA
                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MEERYYPVIFPDERNFRPFTSDSLAAIEKRIAIQKERKKSKDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAEPOPRPOLDLKASRKLPKLYGDIPPELVAKPLEDLDPFYKDHKTFMVLNKKRTIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 5905)
Dib-Hajj.S.D., Tyrrell,L., Black,J.A. and Waxman,S.G.
MaN, a novel voltage-gated Na channel, is expressed preferentially in peripheral sensory neurons and down-regulated after axotomy proc. Natl. Acad. Sci. U.S.A. 95 (15), 8963-8968 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF059030 5905 bp mRNA ROD 16-JUL-2001 status norvegicus voltage-gated Na channel alpha subunit NaN mRNA, complete cds.
AF059030. GI:14719821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 5905)
Dib-Hajj,S.D., Tyrrell,L., Black,J.A. and Waxman,S.G.
Direct Submission
Submitted (10-APR-1998) Neurology, Yale University Medical School, 333 Cedar St, New Haven, CT 06510, USA on Jul 16, 2001 this sequence version replaced gi:3372614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                     /product="voltage-gated Na channel alpha subunit NaN"
/protein_id="AAC40199.1"
/db_xreff="G1:3372615"
                                                                                                                                                                    tgagggtgaagatggatgacagatgctacccagtaatcttccagatgagcggaatttcc 129
                                                                                                                                      Gaps
                                                                                                                                                                                                    72
                                                                                                                                                                                      13 TCAGGGTGAAGATGGAGAGAGAGATACTACCCGGACCAGCGGAATTTCC
                                                                                                                                                                                                                                                                                                                         133 GGAAGAAGTCCAAAGACAAGGCGCAGCTGAGCCCCAGCCTCGGCCTCAGCTTAA
                                                                                                                                                                                                                                                                                                         aaaagaagtctaaagaccagacaggagaagtaccccagcctcaacctcagcttgacctaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="TTX-R voltage-gated Na channel;
tetrodotoxin-resistant voltage-gated Na channel"
                                                                                                   Length 5334;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="dorsal root ganglia"
                                                                                                53.6%; Score 160.4; DB 6; ilarity 83.9%; Pred. No. 1.8e-38; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
                                   1382
/organism="unidentified"
/db_xref="taxon:32644"
1338 c 1314 g 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley
/db_xref="taxon:10116"
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                                                                                                  Query Match
Best Local Similarity
Matches 193; Conserv
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TITLE
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REFEŘENCE
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AF059030
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ALDPYHYERHOWNEDSIVALLSLADVLYNTLSDNNRSFLASLRVLRYFKLASKWPTL
NTLIKLIGHSTOGENLTVVLTIVPTESVVGMRLECTKFRKTAYATGERPRRWHMD
NTLIKLIGHSTOGENLENWGCMQDMGSPLCITVFVLIMVIGKLVVLNLFTALLL
NSFSREEKDGSLEGEFRKTKVLALDRERRAFSFMLHALGSFCCKKGRKUSFPKET
TESFAGENKDSILPDARPWKEYDTDMALYTGQAGAPLAPLASCKCRKCRKUSFPKFRY
SQHSAGVQAGDLEPETKQLTSPDAGVEMEVFSEDLHLSOSPRKKSDAVSHLSECS
TIDLNDIFRULQKTVSPKQDRCFRGLSCHFLCHKTDKRKSPWLHWNIRKTCYQI
VKKSWFESFITFYLLLSSGALIFEDVNLDSRRPOYEKLLRCTDNIFTFFLLLENGLMLKWV
AFGFRRYFTSAMCWLDFLIVVVSVLSLMNLPSLKSFTTRALRALRCTALLKATUSK
                                                                                                                                                                                                                                                                                                                                                       QCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANL
YAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQOKKLGGODIFWTEEQKKYYNAMKKLG
TKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                            DILNIAFVVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLYSRLEDSDISF
PPTLFRVVRLARIGRILRLVRAARGIRFLLFALMMSLPSLFNIGLLFLVWFIYAIFG
MSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVW
EKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFQFLVMDLPMVMGDRLHCMDVLFA
FTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKRKEEEQGAAVIQRAYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                            YALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRS
VDPLHRQRALSAVSILTITMQEQEKFQEPCFPCGKNLASKYLVWDCSPQWLCIKKVLR
                                 TIMTDPFTELAITICIIINTVFLAVEHHNMDDNLKTILKIGNWVFTGIFIAEMCLKII
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5858)
Dib-Hajj,S.D., Tyrrell,L., Escayg,A., Wood,P.M., Meisler,M.H. and Waxman,S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coding sequence, genomic organization, and conserved chromosomal localization of the mouse gene Scn11a encoding the sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 AGGGTGAAGATGGAGGAGGAGGTACTACCCGGTGATTCCCGGACGACGAATTTCCGC 102
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Mus musculus voltage-gated sodium channel NaN (Scn11a) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agggtgaagatggatgacagatgctacccagtaatcttccagatgagcggaattccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160; DB 10;
Pred. No. 2.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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ilarity 84.2%;
Conservative
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2 (bases 1 to 5858)
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192; Conserv
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99375324
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TSQPSEEAQACDLPLKTKRLPSPDDHCVEMEVFSEEDPNLTIOSARKKSDAASMLSEC
STIDLNDIFRNLQKTVSPQKQPDRCFPKGLSCIFLCCKTIKKKSPWVLWWNLRKTCYQ
IVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLKCTDNIFTFIFLLEMILKW
VAFGFRKYFTSAWCWLDFLIVVVSVLSLTNLPNLKSFRNLRALRPLRALSQFEGMKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATEPQPROLDLKASRKLPKLYGDVPPDLIAKPLEDLDPFYKDHKTFWVLKKRTIYR
SEKRALELIGGPRDPIRSSDAN
PEYKPIGIYLLGAPUPIRSSDAN ICTVIIONEMANNSSDSRPSSNI
PEYVPIGIYULBAVIKILARGHIYDBFSYLRDPWNWLDFIVGFAIAPCFLGRKVNNL
STLRTFRVLRALKAISVISGLKVIVGALLRSVKKLVDWNVLTLFCLSIFALVGQQLFM
GILSOKCIRODGSPARFSVKDCFVKRNSDEPIRTGGMRGTFRDPD
YNTIRFDSFCWSFLAMFRVWTOSFKRNSDEPIRTGGMRGTFRDPD
TLAVYTMRTSDSFCWSFLAMFRVWTOSFWRINTAGIIYFVFFFVVTFLGSFYLLNL
TLAVVTWAYEGONRNVAAETBAKEKMFQGAQLLREEKKALVDMGIDBTSLNSLAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNALMSAIPAILNVLLVCLIFWLIFCILGVNFFSGKFGRCINGTDINKYFNASNVPNO
SQCLVSNYTWKVPNVNFDNVGNAYLALLQVATYKGWLDIMNAAVDSRGKDEQPAFEAN
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KRROPKPIPERLNKCQAFVPDLVTSQVFDVIILGLIVTNMIIMAMESESGOPNEVKKI
FDILNIVFVVIFTVECLIKFVALRQHSFTNGMNLFDCVVVVIIISTLVSGLENSNVF
PPTLFRIVRLARIGRILKRLVRAARGIFFLLAMMSLDSVLFNIGLLEFLVMFIYAIFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKFDPEATQFIQYSSLSDFADALPEPLRVAKPNRFQFLMMDLPMVMGDRLHCMDVLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEERYYPVIFPDERNFRPFTFDSLAAIEKRITIQKEKKKSKDKA
Dib-Hajj,S.D., Tyrrell,L. anu mammer.
Direct Submission
Submitted (05-JAN-1999) Neuroscience Research Center, 127A, Yale
University/VAMC, 950 Campbell Ave, West Haven, CT 06516, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 gicticigicotgagggigaagaiggatgacagaigciacccagiaaicticcagaigag 119
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                                                                                                                                                                                                                                                              /note="distal segment; close proximity to Scn5a and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product."voltage-gated sodium channel NaN"
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="TTX-R sodium channel"
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); Mismatches
                                                                                                                                                                                      /strain="1CR"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                          /chromosome="9"
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/gene="Scn11a"
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          AUTHORS
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FSAKRALFILGPFNPIRSFMIRISVHSVFSMFIICTVIINCMFMANNSSVDSRPSSNI
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FSPKKRK FFGSKTRK SFFMRGSKTARASASDSEDDASKK PQLLEQTKRLSQNLPVELF
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STLRTFRVLRALKAISVISGLKVIVGALLRSVKKLVDVMVLTLFCLSIFALVGQQLFM
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KIIALDPYHYFRHGWNIFDSIVALVSLADVLFHKLSKNLSFLASLRVLRVFKLAKSWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Ściurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                        AB031389 5921 bp mRNA ROD 23-FEB-2000 Mus musculus mRNA for voltage-gated sodium channel alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogata,K., Jeong,S., Goto,J., Murakami,H., Hashida,H., Suzuki,T., Masuda,N., Hirai,M., Isahara,K., Uchiyama,Y. and Kanazawa,I. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning and expression study of the mouse tetrodotoxin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katsuhisa ógata, Graduáte School of Medicine, The University of Tokyo, Department of Neurology; 7.3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan (E-mail:OGATA-NRU@h.u-tokyo.ac.jp, Tel:+81-3-5800-8672, Fax:+81-3-5800-6548)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="voltage-gated sodium channel alpha subunit
NaT/Scnlla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-1999) to the DDBJ/EMBL/GenBank databases.
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Masuda,N., Hirai,M., Isahara,K., Uchiyama,Y., Goto,J. and
voltage-gated sodium channel alpha subunit NaT/Scnila Biochem. Biochys. Res. Commun. 267 (1), 271-277 (2000) 20090627
                                                                                                                                                                                                                                                                                                                                                                                           voltage-gated sodium channel alpha subunit NaT/Scnlla.
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1. .5921
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Mus musculus
                                                                                                                                                                                                                                                                                              NaT/Scnlla, complete cds.
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JOURNAL
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SQCLVSNHTWKVPNVNFDNVGNAYLALLQVATYKGWLDIMNAAVDSRGKDEQPAFEAN LYAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKL FDILNIVFVVIFTVECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTLVSGLENSNVF PPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFG MSWFSKVKRGSGIDDIFNFDFFSGSMLCLFQITTSAGWDALLNPMLESKASCNSSSQE SCQQPQIAIVYFVSYIIISLLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEIW

GTKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVTNMIIMMAESEGQPNEVQKI

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HMEKNIKLKKGRSSQLOVFCKOMBLSSLDVPKIKVHCD"
1447 c 1396 g 1548 t
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NTLIKIIGHSVGALGANLTVVLTIVRFIFSVGARLFFOTKFNKTAYATGERPRRHMD
NFYHSFLVVFRILCGEWIENNMGCMQDMDGSPLCIIVFVLINWIGKLVVLNLFALLL
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TESFAGENKDSILPDARPWKEYDTDWALYTGQAGAPLAPLAEVEDDVEYCGEGGALPT
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TIDLNDIFRNLQKTVSPKKQPDRCFPKGLSCHFLCHKTDKRKSPWVLWWNIRKTCYQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                               cggaatttccgcccttcacttccgactctctgctgcaattgagaagcggattgccatc 179
                                                                                                                                                                                                                                                                                    gtctctgtcctgagggtgaagatggatgacagatgctacccagtaatctttccagatgag 119
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 CAAAAGGAGAAGAAGAAAGAAAGACAAGGCAGCAGCCCCAGCCTCGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                          150 AGGAATTTCCGCCCCTTCACTTTCGACTCTTTGGCTGCAATAGAGAAGCGGATCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caaaaggagaaaaagaagtctaaagaccagacaggagaagtaccccagcctcaacctcag
                                                                                                                                                                              Length 5921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1) CTCGACCTAAAGGCCTCCAGGAAGTTACCTAAAGCTCTATGGCGACGTTCCCC 321
                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                              DB 10;
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Tate, S.N., Grose, D.T. and Hick, C.A.

Mammalian sodium channel proteins

Patent: Wo 9947670-A 1 23-SEP-1999;

TATE SIMON NICHOLAS (GB); GLXXO GROUP LTD

(GB); HICK CAROLINE ANNE (GB)
                                                                                                                                                                              Score 159.2; DB 10;
Pred. No. 4.3e-38;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N Sequence 1 from Patent W09947670. AX017217 1 GI:100.
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                                                                                                                                                                              53.2%;
llarity 83.2%;
Conservative
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Matches 193;
                                                                                                                                                                                Query Match
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AX017217
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SOURCE
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CCIISNYSWKVPQVNPDNVGNNYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANL
YAYLYEVVFIJEGSFTLNLFIGVIIDNFNQQKKLGGQDIFMTEEGKKYYNAMKKLG
YKKRQKPIPRLNKCQAFVFDLVTSQVFDVIILGLIVLNMIINAAESAOQPKDYKTF
DILMFRVYIFTIECLIKVFALRQHYFTNGWNLFDCVYVVISIISTLYSKESDSDISF
PPTLFRVYRLARIGRILRLYRARGIFFLLEAMMSLPSLFNIGLLFLVWFIYAIFG
MSWFSKYKKGSGIDDIENFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQD
                                                                                                                                                                      SCOOPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVW
EKFDPEASOFIQYSALSDFADALPEPLRVAKFNKFOFLVMDLPMVMGDRLHCMDVLFA
FTRYULGDSGLDTMKTMMERFKMEANPFKKLYEPIVTTKRKEEEGGAAVIQRAYRK
HMEKNWKLRKLADRSSSHQVFCVNGDLSSLDVAKVKVHND"
1471 c 1435 g 1517 t
                AFGFRRYFTSAWCWLDFLIVVVSVLSLMNLPSLKSFRTLRALRPLRÅLSQFEGMKVVV
YALISAIPAILINVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRS
                                                                                                                                                                                                                                                                                                                                                                         ;
VKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCTDNIFTFIFLLEMILKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-APR-1999) Tate S.N., Molecular Pharmacology, GlaxoWellcome Research and Development, Medecines Research Centre, Gunnels Wood Road, Stevenage, Hertfordshire, SGI 2NY, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostom1;
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                                                                                                                                                                                                                                                                                                                                                                                                            72 agggtgaagatggatgacagatgctacccagtaatctttccagatgagcggaatttccgc 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccettcacttccgactctctggctgcaattgagaagcggattgccatccaaaaggagaaa 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tate, S., Benn, S., Hick, C., Trezise, D., John, V., Mannion, R.J., Costigan, M., Plumpton, C., Grose, D., Gladwell, Z., Kendall, G., Dale, K., Bountra, C. and Woolf, C.J.
Two sodium channels contribute to the TTX-R sodium current in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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channel alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 AAGAAGTCCAAAGACAAGGCGGCAGCTGAGCCCCCAGCCTCGGCCTTGACCTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGTGAAGATGGAGGAGGAGTACTACCCGGTGATCTTCCCGGACGAGCGGAATTTCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aagaagtctaaagaccagacaggagaagtaccccagcctcaacctcagcttgacctaaag
                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                   Length 5897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sodium channel.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNO237852 5849 bp mRNA ROD Rattus norvegicus mRNA for voltage-gated sodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="dorsal root ganglia"
1. 5298
                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                              Score 158.4; DB 6
Pred. No. 7.5e-38;
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alpha subunit; sns2 gene; voltage-gated
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Nat. Neurosci. 1 (8), 653-655 (1998)
99212311
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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83.8%;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                     191; Conservative
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AJ237852
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PNO237852
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DEFINITION
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: TITLE
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Euteleostomi;

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DILNIARYVIFTIECLIKVFALRQHYFTNGWNLFDCVVVVLSIISTUSELEDSDISF
PPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLFLVWFIYAIFG
MSWFSKVKKGSGIDDIENBETPFGSMLCLFQITTSAGNDTLLNRMLERAKEHCNSSSQD
SCQQDQIAVVYEVSIIISFLIVWNTAVILENFWTATESEDELGEDDFEIFYEVW
EKFDPRASQFIQYSALSDFADALDEDLEVARRNKFQFLYMDLDHVMGBRLHCMNDLFR
FTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTKRKBEEGGAAVIQRAYR
                                                                                                                                                       AAEPQPRPQLDLKASRKLPKLYGDIPPELVAKPLEDLDPFYKDHKTFMVLNKKRTIYR
                                                                                                                                                                         FSAKRALFILGPFNPLRSLMIRISVHSVFSMFILCTVIINCMFMANSMERSFDNDIPE
YVFIGIYILEAVIKILARGFIVDEFSFLRDPWNWLDFIVIGTAIATCFPGSQVNLSAL
                                                                                                                                                                                                              RTFRVFRALKAISVISGLKVIVGALLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGIL
NQKCIKHNCGPNPASNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNDDNNY
TKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLA
                                                                                                                                                                                                                                                                                          KKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTKRLSQNLPVDLFDEH
VDPLHRQRALSAVSILTITMQEQEKFQEPCFPCGKNLASKYLVWDCSPQWLCIKKVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFGFRRYFTSAWCWLDFLIVVVSVLSLAMNLPSLKSFRTLRALRPLRALSQFEGMKVVV
YALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANL
YAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFWTEEQKKYYNAMKKLG
                                                                                                                                    /translation="MEERYYPVIFPDERNFRPFTSDSLAAIEKRIAIQKERKKSKDKA
                                                                                                                                                                                                                                                                         VVTMAYEEQNRNVAAETEAKEKMFQEAQQLLREEKEALVAMGIDRSSLNSLQASSFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKKPQKPIPRPLNKCQAFVFDLVTSQVFDVIILGLIVLNMIIMMAESADQPKDVKKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF117907 5874 bp mRNA PRI 18-MAY-1999 (SCN10A) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 atggatgacagatgctacccagtaatctttccagatgagcggaatttccgcccttcact 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 tccgactctctggctgcaattgagaagcggattgccatccaaaaggagaaaaagaagtct 200
                                                                           /product="voltage-gated sodium channel alpha subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMEKMVKLRLKDRSSSHOVFCNGDLSSLDVAKVKVHND"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aagttgcccaa-ctctatggcgacaatcctcggaggctt 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 151; DB 10;
Pred. No. 1.4e-35;
); Mismatches 35;
                                                                                              /protein_id="CAB41850.1"
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83.6%;
'gene="sns2"
                                  /gene="sns2"
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Best Local S
Matches 183
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TVIYTFEALIKILARGFCLNEFTYLRDPWNWLDFSVITLAYVGTAIDLRGISGLRTFR
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LAVVTWAYEEQNQATTDEIEAKEKKFQEALEMLRKEQEVLAALGIDTTSLHSHNGSPL
TSKNASERRHRIKPRVSEGSTEDNKSPRSDPYNQRRMSFLGLASGKRRASHGSVFHFR
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BEHQPPPTSELAPGANUVSAFDAGGWTELASRTLDEPRAGRAMSVSITSVLEEL
BESEGKCPPCLTSLGOCCPMWYKITLAGTUPPFABLITIT.CIVWNITEM
AMEHHGMSPTFEAMLOIGNIVFIFFTAEMVFKIIAFDYYTFGKWNIPDCIIVTVS
LLELGVAKKSSLSVLRSFRLAVFKLAKSWPTLATIKIIGNSVGALGMITIILAIIV
FVFALVGKOLLGENYRNINKNISAPHEDWPRHHHDFFHSFLIVFRILGEWIENMA
CMEVGGKSICLILFLTVWVLGNLVVLNIFTALLNSFSADNLTAPEDDGEVNNLQVAL
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GAQAPRENDEHDFTANTWVSVPTARGESDLDLEDDGEDDGGEDAGVEQQEVIPKGQ
EOLQQVPERCGDHLTPRSPGTGTSSEDLARSLGETWKDBSVPQARAGVDDTSSSEGST
VDCLDPEEILRKIPELADDLEEPDDCFTEGCIRHCPCCKLDTTKSPWDVGWQVRKTCY
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VPLSIVNNKSDCKIQNSTGSFFWVNVKVNFDNVAMGYLALLQVATFKGWMDIMYAAVD
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PILNTGPPYCDPNLPNSNGTRGDCGSPAVGIIFFTTYIIISFLIVVNMYIAVILENFN
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ATLAWKQEDISATVIQKAYRSYVLHRSMALSWTPCVPRAEEEAASLPDEGFVAFTAN
ENCYLPPGSTASATSFPSYSEVYRGLSDRVNMRTSSSIQNEDEATSMELIAPGP"
1552 c 1428 g 1460 t
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/translation="MEFPIGSLETNNFRRFTPESLVEIEKQIAAKQGTKKAREKHREQ
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VKNDMAVNETINYSSHRKPDIYINKRGTSDPLLCGNGSDSGHCPDGYICLKTSDNPDF
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VETDDQSEEKTKILGKINQFFVAVFTGECVMKMFALRQYYFTNGWNVFDFIVVVLSIA
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                                                                                   Rabert, D.K., Koch, B.D., Ilnicka, M., Obernolte, R.A., Naylor, S.L., Herman, R.C., Eglen, R.M., Hunter, J.C. and Sangameswaran, L. A terrodotoxin-resistant voltage-gated sodium channel from human dorsal root ganglia, hPN3/SCN10A
Pain 78 (2), 107-114 (1998)
                                                                                                                                                                                                                                                                        Rabert, D.K., Koch, B.D., Ilnicka, M., Obernolte, R.A., Naylor, S.L., Herman, R.C., Eglen, R.M., Hunter, J.C. and Sangameswaran, L. Direct Submission
Submisted (05-JAN-1999) Target Identification, Roche Bioscience, 3401 Hillview, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="tetrodotoxin-resistant voltage-gated sodium
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   Craniata; Vertebrata; I
Catarrhini; Hominidae;
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/tissue_type="dorsal root ganglia"
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Pred. No. 0.0031;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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Chordata;
Primates;
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Similarity 60.7%;
99; Conservative
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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RFAATALLES PENLITRITAIK VS VHSWELFIT VIT LIV NCV OMTOTEL DER LETYF
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VERALKTSVIT DELKVIV OG LIHSVEKLADVTILIT VECLSYFALL OG LEKGENER KKK
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LKTSN NADENT SEPSER WARTER OND SWERLY OG TLEAR SGRYYW VERVIT LEAN SER MAY REGONDATIDEIER KEKT FOETLEMPRE GEVLAALGID TAS
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CIVVNTVFWAMEHHGMSSAFBAMLQIGNIVFTVFFTAEMVFKIIAFDPYYYFQKRWNI
FDCIIVTVSLIELGAARKGSLSVLRTFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGN
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GEWIENMWRACWEVGQKSICLILFLYVWVLGNLVVLNLFTALLLNSFSADNLATPDEDG
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VWRTCYRTVTVBHSWFEBFITEMILLSSGSLAREDSHLDOKPVTKALLEFTDRMFFFIF
VLEMLLKWYAYGFKFTVAMCWLDFLIVUNISLISLIAKILQYSDVASIKALFRIRAL
RPLRALSRFEGMRVVVDALVGAIPSIMNVLLVCLIFWLIFSTMGVNFFAGKFGRCINK
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IMYAAVDARDVNLQPKWEDNVYMYLYFVIFIIFGGFFTLNLFVGVIIDNFNQQKKKLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l (bases 1 to 6726)
Chen, J. Ikeda, S.R. Lang, W., Isales, C.M. and Wei, X.
Molecular cloning of a putative tetrodotoxin-resistant sodium channel from dog nodose ganglion neurons
Gene 202 (1-2), 7-14 (1997)
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                                      aatttccgccccttcacttccgactctcggctgcaattgagaagcggattgccatccaa
                                                                                                                                                                                        -----cagacaggagaagtaccccagcct
                                                                                                                                                                                                                                                                     94 CAGGGAACAAAGAAAGCCAGAGAGGAAGCATAGGGAGCAGAAGGACCAAGAAGAAGAAGCCT
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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/db_xref="G1:2760341"
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LPALENIGLLIELVMFIYSIFGMASFPHVSWEAGIDDMFNFQTFANSMLCLFQITTSA
GWDGLLSPILMTGPPYCDPNLPNSNGSRGNGGSPAVGILFFTTYIIISFLIVVNMYIA
VILENFNVATQESSEPLSEDDFDMFYETWEKFDPEATQFITFALSDFADTLSGPLRI
PKPNQNILLQMDLELVPGFN HCLDLIFAFTKNVLGESGELDSLKANIEEKFWATNVS
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VEFMVNENCALPDKSETASAASFPPSYDSVTRGLSDQINMSTSSSMQNEDEGTSKKVT
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VVVLSIGSLVFSVILTSLENYFSPTLFRVIRLARIGRILRLIRAAKGIRTLLFALMMS
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GODI FMTEEOKKYY NAMKKLGSKK POKPI PRPLNKY OGFVFDI VTKOAFDIV IMVLIC
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Homo sapiens PAC clone RP6-91H8 from 14q24.3, complete sequence.
AC004817
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Submitted (14-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Web site: http://genome.wustl.edu/gsc
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Dec 21, 1999 this sequence Version replaced 91:4156208.
                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                DB 4; Length 6726;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                  Indels
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The sequence of Homo sapiens PAC clone RP6-91H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.8%; Score 44.2; DB 4;
llarity 60.1%; Pred. No. 0.0097;
Conservative 0; Mismatches 53;
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Submitted (12-JUN-1998) Genome
University School of Medicine,
MO 63108, USA
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3 (bases 1 to 128398)
Waterston, R.H.
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Waterston, R.H.
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Mammalia; Eutheria; Pr
1 (bases 1 to 128398)
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 14 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR14, send
                                                                                                                                                                                                                                                                                                                                                            all regions were double stranded, sequenced with an alternate chemistry. or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone was derived from human PAC library RPCI-6, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one female donor. For further details, see http://bocpac.med.buffalo.edu/
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                                                                                                                                                                       not represent the entire insert of this
                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted:
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DA0091H08
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/chromosone="14"
/map="14424.3"
/clone="RP6-91H8"
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567. .1816
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2892

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/rpt_family="(TAAA)n"
15840. .16135
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24963. .24989
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9731. .9860
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13954. .13990
/rpt_family="U2"
14008. .14472
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1530, 11560
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13261. .13541
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7139. 1771.
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.5197. .15512
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TYTYTPEALK IL RICHSFTLINEYDWNWLDFSYTLAYVGAAIDLRGISCLRFT
VLRALKTVSVIPGLAKFCLNETYLEWRALDPVTILTVFVTLSYVGAIDLRGISCLRFTF
TROGTDPHKADNLSSEMAEXIFIKPGTTDPLLCGNGSDAGHCPGGYVCLKTPDNPDFN
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ARIQVLGHRASRAIASYISSHCRFRWPKVETQLGMKPPLTSSEAKNHIATDAVSAAVG
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ION CRANNEL
Batent: WO 9701577-A 7 16-JAN-1997;
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                                                                                                                                                                                                                                                                                                      Score 38.6;
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/db_xref="GI:3714381"
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26927, 27125
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                   /rpt_family="MaLR"
26333. .26460
                                                         /rpt_family="Alu"
26460. .26532
                                                                                             /rpt_family="Alu"
26533. .26770
                                                                                                                                      /rpt_family="Alu"
26773. .26805
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LESPEGMRYVDALVGAIPSIMVNLYCLIFWLIESIMGVYLLRAGKFSKOYDTRNDP
SINNSTYMVNIK SECHRONSTGHFFWNNYKYNEDNVAGYLALLOYAFRGWND MYAA
VDSGEINSQPNWENNLYRYLYFVVFIIFGGFFTLINLFVGVIIDNFNQOKKKLGGQDIF
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LSPILNTGPPYCDPNLPNSNGSRGNCGSPAVGIIFFTTYIIISFLIVVNMYIAVILEN
                                                                                                                                                                                                                                                                                          FNVATEESTEPLSEDDFDMFYETWEKFDPEATQFIAFSALSDFADTLSGPLRIPKPNQ
NILIQMDLPLVPGDKIHCLDILFAFTKNVLGESGELDSLKTNMEEKFMATNLSKASYE
                                                                                                                                                                                                          IGSLLFSAILKSLENYFSPTLFRVIRLARIGRILRLIRAAKGIRTLLFALMMSLPALF
CYRIVEHSWFESFIIFMILLSSGALAFEDNYLEEKPRVKSVLEYTDRVFTFIFVFEML
                                                                                                                                                MTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFVFDIVTRQAFDIIIMVLICLNMIT
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llarity 62.5%; Pred. No. 0.59;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Ouery
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| 24 | 31.4 | | 483 | 0 | AAH55766 | SCNIA |
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| | 3.1 | 0 | 13425 | 16 | AAV52284 | |
| 27 | 0 | 10.2 | 481 | 20 | AAZ06952 | Rice cyclopropane |
| | 30.4 | 0 | 1951 | 22 | AAC92291 | Human pollinosis-a |
| | 0 | 0 | 3442 | 22 | AAC92313 | Human pollinosis-a |
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| | 0 | 0 | 6219 | 20 | AAV82500 | Calcium permeable |
| | 0 | 0 | 1025 | 22 | AAH55828 | Human SCN3A genomi |
| | 0 | ٥. | 1066 | 19 | AAV53410 | DNA encoding a bio |
| | 0 | 0. | 9112 | 22 | AAH55823 | Human adult form o |
| 36 | ö | 0 | 9112 | 22 | AAH55824 | Human neonatal for |
| | 6 | ٥. | 558 | 22 | AAH10196 | Human cDNA clone (|
| | 29.8 | o. | 4054 | 20 | AAX13188 | Enterococcus faeca |
| 68. | 6 | • | 531 | 21 | AAA69707 | Human ovarian carc |
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| 43 | 6 | | 3834 | 22 | | Human alpha nicoti |
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Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss. Human sensory neurone specific 2a nucleotide sequence fragment #1. Tate SN; 98GB-0005793. 99WO-GB00838. (first entry) (GLAX) GLAXO GROUP LTD Grose DT, Hick CA, WPI; 1999-562112/47. saptens. W09947670-A1. 18-MAR-1999; 18-MAR-1998; 03-DEC-1999 23-SEP-1999 AAZ21481; Homo

Mammalian sodium channel protein for treating pain and hypersensitivity

AAZ21481 to AAZ21495 represent fragments of the human sensory neurone

Claim 6; Page 66; 73pp; English.

'n,

Claim 1; Fig 11A; 162pp; English.

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specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity.
                                                                                                                                                    241 ttgacctaaaggcctccaggaagttgcccaactctatggcgacaatcctcggaggcttt 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                 ggaatttccgcccttcacttccgactctctggctgcaattgagaagcggattgccatcc
                                                                                                                               ;
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                                                                    Sequence 299 BP; 74 A; 81 C; 73 G; 71 T; 0 other;
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The present sequence is that of cDNA encoding a novel human tetrodocoxin resistant sodium channel, termed NaN (see AAB20121).

The cDNA was isolated from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also AAF30122-23). NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTY-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a correct useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an expension of that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant procession of NaN mand in the recombinant procession or the diagnose, and in the recombinant procession or procession or (antisense) to down-regulate the page of the procession or (antisense) to down-regulate the procession or (antisense) to down-regulate the page of the procession or (antisense) to down-regulate the procession or (antisense) to down-regulate the procession or the diagnosis of disease, and in the recombinant the page of the procession or (antisense) to down-regulate the procession or the diagnosis of disease, and in the recombinant the page of the procession or (antisense) to down-regulate the procession or the page of the procession or (antisense) to down-regulate the procession or (antisense) to down-regulate the procession or (anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 5860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "these bases represent nucleotides missing from the sequence given in Fig 1 of the specification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 tcagggtgaagatggaggaggaggtactacccggtgatcttcccggacgagcggaatttcc
                                                                                                                                                                                                                                                                                                                             The present sequence encodes a type 5 sodium channel protein designated PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX) The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5334;
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83.9%; Pred. No. 1.1e-41;
ive 0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 agatgagcggaatttccgcccttcacttccgactctctggctgcaattgagaagcggat 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 gootcagottgacotaaaggootcoaggaagttacotaagotttatggtgacattococo 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stabilised cDNA encoding type 5 sodium channel protein designated PN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgccatccaaaaggagaaaaagaagtctaaagaccagacaggagaagtaccccagcctca
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                                                                                                                                                                                                                                                                                                   The present sequence encodes a type 5 sodium channel protein designated PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root gangila. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, tranmatic injuries, AnDS-related neuropathy, and especially neuropathic pain, e.g. migraine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy; neuropathic pain; migraine; headache; ss.
                                                       ä
                                                       Sangameswaran
                                                                                                                                                                                             Isolated DNA encoding sodium channel of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5908 BP; 1458 A; 1474 C; 1451 G; 1525 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 167.8; DB 20;
Pred. No. 4.5e-44;
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                                                       Rabert DK,
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(HOFF ) HOFFMANN LA ROCHE & CO AG
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                                                                                                                                                                                                                                                 Fig 1A-E; 90pp; French.
                                                    Khare
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al Similarity 82.6%;
204; Conservative
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P-PSDB; AAY16572.
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                                                       Dietrich PS,
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Rattus sp. Synthetic

AAX60244;

AAX60244

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of an isolated nucleic acid which encodes the rat NaN channel (see AAY06596), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel CDNA was obtained from Sprayue-DBALPY at DRG CDNA by PCR and RACE amplification (see also AAX87600-17). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAX87609-98) are provided. The invention also includes expression vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccettcaettccgaetctctggctgcaattgagaagcggattgccatccaaaaggagaaa 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provider. In the invention also includes explession vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The NaN gene has been named Scnlla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 aagaagtctaaagaccagacaggagagagtaccccagcctcaacctcagcttgacctaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 160; DB 20; Length 5875; ilarity 84.2%; Pred. No. 1.5e-41; Conservative 0; Mismatches 35; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 52 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-D; 91pp; English
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                                                                 99WO-US02008
                                                                                                98US-0109402
98US-0072990
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                                                                                                                                                                               Dib-Hajj S, Waxman S;
                                                                                                                                                                                                                 WPI; 1999-479168/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                  (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                  P-PSDB; AAY06596
WO9938889-A2.
                                                               29-JAN-1999;
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                              05-AUG-1999
                                                                                                                                                                                                                                                                                                    phenomena
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AAF30102
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Rat sodium channel NaN cDNA.
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Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.

Rattus norvegicus.

Location/Qualifiers 41..5338 /*tag=

WO200105831-A1

25-JAN-2001.

14-JUL-2000; 2000WO-US19342.

99US-0354147. 16-JUL-1999;

(UYYA) UNIV YALE.

Waxman SG; Dib-Hajj S,

P-PSDB; AAB20122, AAB20123. WPI; 2001-103147/11

Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -

Example 1; Fig 1; 162pp; English.

The CDNA was isolated from a dorsal root ganglia tissue CDNA library by PCR amplification using generic primers (from conserved library by PCR amplification using generic primers (from conserved library by PCR amplification using generic primers (from conserved primers (see also AAR30105-19), and RACE amplification. The copen reading frame shows 73% similarity to the human NaN sequence (see AAR30101). NaN belongs to the a-subunit voltage-gated sodium channel protein family and propagation of impulses in channel protein family and propagation of impulses in channels underlie the generation and propagation of impulses in channels underlie the generation and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or continents. The present sequence is that of cDNA encoding a novel rat tetrodotoxin resistant sodium channel, termed NaN (see AAB20122). disease, and in the recombinant production of NaN polypeptides.

Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 2 other;

Gaps 1; Length 5875; Indels 35; 53.5%; Score 160; DB 22; 84.2%; Pred. No. 1.5e-41; ive 0; Mismatches 35; Query Match 53.5 Best Local Similarity 84.2 Matches 192; Conservative

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72 agggtgaagatggatgacagatgctacccagtaatctttccagatgagcggaatttccgc 131

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalian sodium channel protein for treating pain and hypersensitivity
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s specific 2a; SNS-2a; sodium channel protein; pain; hypersensitivity; ss.
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                                                                           /*tag= a
/product= "sensory neurone specific 2a"
                                                                                                                                                                                                                                                                                                                        Rat sensory neurone specific 2a nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
49..5346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 52-58; 73pp; English.
                                                                                                                                                                                                            BP.
                                                                                                                                                                                                          AAZ21480 standard; cDNA; 5897
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P-PSDB; AAY41668.
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Matches 191
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This is the nucleotide sequence of an isolated nucleic acid which encodes the mouse NaN channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from mouse trigeminal ganglia cDNA by PCR amplification using rat NaN-based primers (see AAX87600-02) and polypeptides (see AAX06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells

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Claim 1; Fig 7A1-3; 91pp; English.

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New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                    These bases represent nucleotides missing from the sequence given in Fig 7 of the paperification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                      NaN; sodium channel; ion transport; mouse; dorsal root ganglia; pain; paraesthesia; hyperexcitability; therapy; Scnlla gene; ss;
Location/Qualifiers
19..5316
                                                        BP.
                                                       AAX87601 standard; cDNA; 5822
                                                                                                       Mouse sodium channel NaN cDNA.
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4201..4260
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98US-0072990
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P-PSDB; AAY06597.
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29-JAN-1998;
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06-FEB-2001
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                                                                                                                                                   63 tctgtcctgagggtgaagatgatgacagatgctacccagtaatctttccagatgagcgg 122
                                                                                                            aatttocgcccttcacttccgactctctggctgcaattgagaagcggattgccatccaa 182
                                                                                                                                           aaggagaaaaagaagtctaaagaccagacaggagaagtaccccagcctcaacctcagctt 242
                                                                Gaps
while not affecting other nerve cells in the brain and spinal cord. The gene encoding NaN has been named Scnlla.
                                                                                                                   Sodium channel; NaN; Scnlla; mouse; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
                                              Length 5822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human tetrodotoxin resistant schannels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of cDNA encoding a novel mouse
                       Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 61 other;
                                                                                                                                                                          52.8%; Score 157.8; DB 20; Length 83.4%; Pred. No. 7.7e-41; ive 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
19..5316
                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                               AAF30103 standard; cDNA; 5822
                                                                                                                                                                                                                                                                             Mouse sodium channel Nan cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2000; 2000WO-US19342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0354147
                                                                                                                                                                                                                                                                                                                                                           /*tag= a
5789..5794
/*tag= b
5800..5822
/*tag= c
                                                                                                                                                                                                                                                              30-APR-2001 (first entry)
                                              Query Match
Best Local Similarity 83.4'
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 7A; 162pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dib-Hajj S, Waxman SG;
                                                                                                                                                                                                                                                                                             Sodium channel; NaN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-103147/11.
P-PSDB; AAB20124.
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                                                                                                                                                                                                                                                                                                                                                                                                        WO200105831-A1
                                                                                                                                                                                                                                                                                                             diagnosis; ss
                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                  polyA_site
                                                                                                                                                                                                                                                AAF30103;
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                                                                                                                                           183
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                                                                                                                                                                                                                         AAF30103
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Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit; tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; human; sodium channel protein; peripheral nervous system; allodynia; neuropathy; hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerary; analgesic; anti-HIV; ss.
tetrodotoxin resistant sodium channel, termed NaN (see AAB20124).

The CDNA was isolated from trigeminal ganglia CDNA using primers (see AAB20120-12) based on rat NaN sequences. Mouse NaN shows to the Samilarity to human NaN (see AAB20121). The gene encoding NaN, termed Scnlia, is located on mouse chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal corriging the body (dorsal root ganglia) and the face (trigeminal corriging pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (animal channels) to down-regulate NaN expression, in the diagnosis of carrect cannels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 tctgtcctgagggtgaagatggatgacagatgctacccagtaatctttccagatgagcgg 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aatttccgccccttcacttccgactctctggctgcaattgagaagcggattgccatccaa 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggagaaaaagaagtctaaagaccagacaggagaagtaccccagcctcaacctcagctt 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 aaggagaagaagaaatccaaagacaaggcagcaactgagccccagcctcggcctcagctc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 52.8%; Score 157.8; DB 22; Length 5822; Best Local Similarity 83.4%; Pred. No. 7.7e-41; Matches 191; Conservative 0; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, and in the recombinant production of NaN polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..5871
/*tag= a
/product= "hPN3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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09-OCT-1997
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                                  Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                        The invention provides purified and isolated rat and human peripheral nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins. The rat peripheral nerve sodium channel 1973 (PN3) protein or its human homologue are useful for the development of antibodies against PN3 which are useful in affinity chromatography to purify recombinant sodium channel proteins or polypeptides, or as a research tool. The PN3 proteins are useful as therapeutic targets for compounds to treat disorders of the peripheral nervous system such as allodynia, hyperalgesia, diabetic eneropethy, traumatic injury and acquired immunodeficiency syndrome encoding the human hPN3 protein.
                                                                                                                        New rat and human tetrodotoxin-resistant, voltage-gated sodium channel proteins, present in peripheral nerve tissue, useful as a therapeutic target for compounds treating peripheral nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaggagaaaaagaagtctaaagac-----cagacaggagaagtaccccagcct 230
                                                                                                                                                                                                                                                                                                                                                                                                                aatttecgeeeetteaetteegaetetetggetgeaattgagaageggattgeeateeaa 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 cagggaacaaagaaagccagagaagcatagggagcagaaggaccaagaagaagagct 153
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Terodotoxin-resistant sodium channel alpha-subunit protein; dog; modose ganglion; NaNG; pain; vagus nerve; spinal accessory nerve; hypoglossal nerve; superiox cervical ganglion; sympathetic trunk; anesthetic; pain killer; ss.
                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                    Length 5874;
                                                                  Sangameswaran L, Rabert DK;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                 Sequence 5874 BP; 1434 A; 1553 C; 1428 G; 1459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 cggccccagctggacttgaaagcctgcaaccagctgcccaagt 196
                                                                                                                                                                                                                                                                                                                                                                 Score 45.8; DB 22;
Pred. No. 0.00013;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caacctcagcttgacctaaaggcctccaggaagttgcccaact
                                                                                                                                                                     Disclosure; Fig 5A-K; 86pp; English
                                                                  Fish LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NaNG polypeptide encoding DNA
                                                                                                                                                                                                                                                                                                                                                                    15.3%;
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 97US-0843417
                      95US-0511828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0066217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                  Herman R, Delgado SG,
                                            (SYNT ) SYNTEX USA INC
                                                                                      WPI; 2001-202004/20.
P-PSDB; AAB61996.
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-1999
15-APR-1997;
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                      11-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX60872;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The invention relates to a terodotoxin-resistant sodium channel alphasubunit protein from dog nodose ganglion (NaNG). The CDNA and encoded proteins are useful in the study of pain and screening for compounds which modulate pain. The terodotoxin-resistant sodium channel (NaNG) is unusual in that it is expressed specifically in nodose ganglia which are at the trunk of the vagus nerve, making connections with the spinal accessory nerve, hypoglossal nerve and the superior cervical ganglian of the sympathetic trunk. Therefor NaNG is a unique target for compounds involved in regulations of pain. Compounds can be screened in vivo or in vitro using standard techniques to screen for local anesthetics and pain vitro using standard techniques to screen for local anesthetics and pain killers. The present sequence represents the nucleotide sequence of NaNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 aattteegeeeetteaetteegaetettggetgeaattgagaageggattgeeateeaa 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 caggcagcaaagaaaagcaaaaggtaagcacagggagcagaaggaccaagaagaagagact 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 aaggagaaaaagaagtctaaa-----gaccagacaggagaagtacccagcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                      New mammalian tetrodotoxin-resistant sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6606 BP; 1651 A; 1696 C; 1597 G; 1662 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 caacctcagcttgacctaaaggcctccaggaagttgcccaact 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.8%; Score 44.2; DB 20;
Best Local Similarity 60.1%; Pred. No. 0.00046;
Matches 98; Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= Variant_Rat_DRG(SNS-B)
   RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding variant rat DRG (SNS-B) #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 3A-G; 36pp; English.
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(MEDI-) MEDICAL COLLEGE GEORGIA
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                                                                               Lang
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                                                                                                                                                   WPI; 1999-357836/30.
P-PSDB; AAY17250.
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                                                                               Ikeda SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rattus.
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/*tag= c /label= G>A /note= "Causes Val > Ile substitution"

/*tag= b /label= C>G

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Gaps

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Indels

Score 38.4; DB 18; Pred. No. 0.035; 0; Mismatches 36;

183 aaggagaaaaagaagtctaaagaccagacaggagaa 218

Length 6527;

1 712

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123 aattteegeeeetteaetteegaetetetggetgeaattgagaageggattgeeateeaa 182
                                                                                                                                              237 aatttcagacggttcactccagagtcactggcagagatcgagaagcagattgctcac 296
sequence contains 12 nucleotide differences to the wildtype rat DRG(SNS-B) (see also AAT77803) causing nine amino acid changes.
                                        Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T; 0 other;
                                                                                                                                                                                                  Query Match 12.8%;
Best Local Similarity 62.5%;
Matches 60; Conservative (
                                                                                                                                                                                                                                                  RESULT 13
    SSXS
                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (paralsympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated mammalian sensory neuron sodium channel protein - used to identify modulators of the sodium channel, partic. for the treatment of pain
                            note= "Causes Ser > Phe substitution"
964
                                                                                                                              note= "Causes His > Asp substitution"
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= 1
/label= G>C
/note= "Causes Arg > Thr substitution"
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/label= T>G
/note= "Causes Ile > Ser substitution"
6525..6527
                                                                                                                                                                                                                                                                                                                                                                              'note= "Causes His > Asp substitution"
                                                                                                                                                                                                                                     Ser > Ile substitution'
                                                                                                                                                                                                                                                                                     'note= "Causes His > Arg substitution'
                                                                                                                                                                                   Ser substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= n
/note= "Addition of AAA"
                                                                                                                                                                                   Thr >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 85-93; 128pp; English.
                                                                                                                                                                                                        /*tag= h
/label= G>T
/note= "Causes S
                                                                                                                                                                     /label= A>T
/note= "Causes
                                                                /*tag= e
/label= G>C
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                                                                                                      /*tag= f
/label= C>G
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/label= A>G
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'label= C>T
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/label= C>
                                                                                                                                                         /*tag=
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Akopian AN, Wood JN;
                                                                                                                                                                                               2986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-100165/09.
P-PSDB; AAW21740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9701577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-1997
  mutation
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                                                                                         mutation
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The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteril nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This
                                                                                                                   Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin; modulator; impulse; sensory neuron; acute pain; chronic pain; neuropathic pain; glia; muscle; parasympathetic nervous system; enteric nervous system; central nervous system; dorsal root ganglia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated mammalian sensory neuron sodium channel protein to identify modulators of the sodium channel, partic. for the treatment of pain
                                                                                                                                                                                                                                                          204..6602
/*tag= a
/product= Variant_Rat_DRG(SNS-B)
                                                                                        cDNA encoding variant rat DRG (SNS-B) #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 69-78; 128pp; English.
                                                                                                                                                                                                                                            Location/Qualifiers
 BP.
AAT77805 standard; cDNA; 7052
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNLO ) UNIV COLLEGE LONDON.
                                                                                                                                                                                                                                                                                                                                                                                 96WO-GB01523.
                                                                                                                                                                                                                                                                                                                                                                                                               95GB-0013180.
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-100165/09.
P-PSDB; AAW21739.
                                                                                                                                                                                   cranial ganglia; ss
                                                                                                                                                                                                               Rattus rattus.
                                                                                                                                                                                                                                                                                                                      WO9701577-A1
                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akopian AN,
                                                          09-0CT-1997
                                                                                                                                                                                                                                                                                                                                                   16-JAN-1997
                              AAT77805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit; tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; rat; sodium channel protein; peripheral nervous system; allodynia; neuropathy; hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerary; analgesic; anti-HIV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New rat and human tetrodotoxin-resistant, voltage-gated sodium channel proteins, present in peripheral nerve tissue, useful as a therapeutic target for compounds treating peripheral nervous system disorders
                                                                                                                                                                                                                                                                                                      aatttoogcocottoaottoogactototggotgoaattgagaagoggattgcoatocaa 182
                                                                                                                                                                                                                                                                                                                                The invention provides purified and isolated rat and human peripheral
                                                                                                                                                                                                                                                   Gaps
ence encodes a 2132 amino acid protein that contains a 176 amino repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)
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                                                                                                                                                                                             Length 7052;
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                                                                                                              Sequence 7052 BP; 1655 A; 2009 C; 1795 G; 1593 T; 0 other;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sangameswaran L,
                                                                                                                                                                                        Score 38.4; DB 18;
Pred. No. 0.036;
); Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                            183 aaggagagaaggagtctaaagaccagacaggagaa 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 cgggcagccaagaaggccagaaccaagcacagagga 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
23..5893
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/product= "PN3"
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                                                                                                                                                                                        / Match 12.8%;
Local Similarity 62.5%;
hes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0843417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat PN3 cDNA sequence.
                                                     (see also AAW21737).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-202004/20.
P-PSDB; AAB61995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-0CT-1995;
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     sequence acid repea
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Best Local S:
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF57009;
                                                                                                                                                                                                                                                                                                      123
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/product= Rat_DRG(SNS-B)

WO9701577-A1

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.6-JAN-1997

/*tag=

96WO-GB01523

25-JUN-1996; 28-JUN-1995; (UNLO) UNIV COLLEGE LONDON

Wood JN;

Akopian AN,

The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel in block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute,

- used

sensory neuron sodium channel protein of the sodium channel, partic. for the

New isolated mammalian to identify modulators treatment of pain

WPI; 1997-100165/09. P-PSDB; AAW21737.

Claim 9; Page 50-58; 128pp; English.

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(AIDS)-associated neuropathy. The present sequence represents the cDNA encoding the rat PN3 protein.
                                                                                                                                                                                                                                                                                                                                                                 tetrodotoxin;
                                                                                                                      ,174 ---gccatccaaaaggagaaaaagaagtctaaagaccagacaggagaagtaccccagcct 230
                                                                                                                                                                          cgcgcagccaagaaggccagaaccaagcacagagacaggagagagagagagagagagagcc 175
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                               Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin modulator; impulse; sensory neuron; acute pain; chronic pain; neuropathic pain; plia; muscle; parasympathetic nervous system; enteric nervous system; central nervous system; dorsal root ganglia;
                                                                Length 6344;
                                                                                      12;
                                Sequence 6344 BP; 1487 A; 1823 C; 1622 G; 1412 T; 0 other;
                                                                                      Indels
                                                                                                          123 aatttocgcccttcacttccgactctcggctgcaattgagaagcggatt
                                                                                                                                                                                                caacctcagcttgacctaaaggcctccaggaagttgcccaact 273
                                                                                                                                                                                                          57;
                                                                22;
                                                                Score 37.8; DB 3 Pred. No. 0.053;
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                          cDNA encoding wild type rat DRG (SNS-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                         AAT77803 standard; cDNA; 6524
                                                                12.68;
57.78;
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              204..6077
                                                                          Best Local Similarity 57.7
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ganglia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus rattus.
                                                                                                                                                                                                                                                                                                                     09-0CT-1997
                                                                                                                                                                                                                                                                                               AAT77803;
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           cranial
                                                                                                                                                                                                                                                    ESULT 15
                                                                                                                                                                          116
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Search completed: February 26, 2002, 22:49:53 Job time: 15273 sec

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Sequence 9, Appli
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version 4.5
- 2000 Compugen Ltd.
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US-08-324-4056-7
US-08-908-733-24
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US-08-870-693-9
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Maximum Match 100%
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Copyright (c) 1993
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Maximum DB seq length: 200000000
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| HH H A A H G W W W W W W A A G G H H | Application US/08843417 6184349 FPORMATION: TT: Herman, Ronald C TT: Herman, Ronald C TT: Sangameswaran, Lakshm: TT: Sangameswaran, Lakshm: TT: Sangameswaran, Lakshm: TT: Rabert, Douglas K INVENTION: TETRODOTOXIN. TT: NUNEWTION: TETRODOTOXIN. THOUSHION: TETRODOTOXIN. FSEE: Heller Ehrman White Palo Alto CA TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY: U.S.A. 94301 TY EBM PC Compatible TY: U.S.A. 94301 TY EBM PC Compatible TY: U.S.A. 94301 TY EBM PC Compatible TY: U.S.A. 94301 TY EBM PC COMPATION: Softwareses, William SATION NUMBER: 31,796 TY TYPE: DO NO: 9: TYPE: CDNA TO NUMBER: 31,796 TYPE: CDNA TO NUMBER: 31,796 TYPE: CDNA | 0.7%; |
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APPLICANT: Taylor, Martin
APPLICANT: Teylor, Martin
APPLICANT: Heckel, David G
TITLE OF INVENTION: Method for Monitoring Pesticide
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                              231 caaceteagettgacetaaaggeeteeaggaagttgeeeaact 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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0; Mismatches
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no. 0646/0A939
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30-DEC-1992
                                                                                                                                                                                                                                                                Sequence 7, Application US/07998289B
Patent No. 6027876
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Sequence 7, Application US/08338702
Patent No. 5550049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Robinson, Joseph R
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.2%;
Best Local Similarity 63.9%;
Matches 46; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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CITY: New York
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APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
                                       123 aattteegeeeetteaetteegaeteetggetgeaattgagaageggattgeeateeaa 182
                                                                                                                    183 aaggagaaaaagaagtctaaagac-----cagacaggagaagtaccccagcct 230
                                                                                                                                                           34 AACTITCCGICGCITIACITCGGAGICACTGGIGGAGAIAGAGAAGCAAAITGCIGCCAAG 93
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  52; Indels
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                                                                                                                                                                                                                                        154 CGGCCCCAGCTGGACTTGAAAGCCTGCAACCAGCTGCCCAAGT 196
                                                                                                                                                                                                    caacctcagcttgacctaaaggcctccaggaagttgcccaact 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: APTIL 15, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.8; DB
Pred. No. 0.003
0; Mismatches
  Mismatches
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                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08843417
Patent No. 6184349
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 12.6%;
1 Similarity 57.7%;
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415)-324-7041
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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Best Local Similarity
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TISSUE TYPE;
; CELL TYPE: P
US-08-843-417-1
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                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-843-417-1
Matches
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APPLICANT: Warmke, Jeffrey W.
APPLICANT: Hall, Linda
APPLICANT: Hall, Linda
APPLICANT: Van Der Ploeg, Leonardus
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEGUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
STREET: P.O. Box 2000 - 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.4; DB 1; Length 6513;
                                SOFTWARE: Patentin Release #1.0, Version #1.25
ADDITOATO. .....
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0; Mismatches
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                                                                                                              APPLICATION NUMBER: US/08/337,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
RECISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application \text{US}/\text{O8724095} Patent No. 5688917
OPERATING SYSTEM: PC-DOS/MG-SOFTHARE: Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.2%;
63.9%;
                                                                                                                                                                                                                                                                                         TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.2'
Best Local Similarity 63.9
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 07065-0907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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Patent No. 5593864
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Hall, Linda
APPLICANT: Feng, Gouping
APPLICANT: Feng, Gouping
APPLICANT: Peng, Gouping
APPLICANT: Prof. Gouping
APPLICANT: Prof. Gouping
APPLICANT: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
                                         APPLICANT: Warmke, Jeffrey W.
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 6513;
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                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,702
                                                                                                                                                                             ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
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Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATORNEY/ACENT INFORMATION:
NAME: WALLEN III, JOhn W.
REGISTRATION NUMBER: 35,403
REFRENCE/DOCKET NUMBER: 19338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
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63.9%;
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Best Local Similarity 63.94
Warches 46; Conservative
                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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US-08-338-702-7
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New Jersey
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                       GENERAL INFORMATION:
APPLICANT: Warmke
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APPLICANT: Hall, Linda
APPLICANT: Feng, Goupin
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PRARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nixon, Hargrave, Devans & Doyle LLP
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Roy D. Meredith
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.4; DB
Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14378
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       Sequence 7, Application PC/TUS9514378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08808793 Patent No. 5858713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,777
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%;
63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6513 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.99
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
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    129 GAAAAGCAGAAG 140
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PCT-US95-14378-7
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STATE: New Jersey
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ZIP: 07065-0907
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                                                                                                     CT-US95-14378-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Warmke, Jeffrey W.
APPLICANT: Wan Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
CORRESPONDENCE: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              Length 6513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6513;
                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14262
                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Jack L. Tribble
P.O. Box 2000, 126 E. Lincoln Avenue
                                                                                                                                                                                Score 30.4; D
Pred. No. 1.3;
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application PC/TUS9514262 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                            10.2%;
nilarity 63.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%;
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
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                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                           129 GAAAAGCAGAAG 140
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PCT-US95-14262-7
                                                                                 linear
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 46; Conserv
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                 ; MOLECULE TYPE:
US-08-724-095-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
PCT-US95-14262-7
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DB 5; Length 6513; Indels

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59 tgtctctgtcctgagggtgaagatggatgacagatgctacccagtaatctttccagatga 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 GCACTACATGCCACTGGCCGATCTATGGGATGTGCTCTACAAGAAGGAATACAATGCTAT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 ccaaaaggagaaaaagaagtctaaagaccagacaggagaagtaccccagcctcaacctca 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 TGTGGCGTCCATGTTGTGAAGCTGGTTGAACTAGGCTTTCTGGTCCCGCTTTCCAACGT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08808793
Patent No. 5858713
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERREABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.7%; Score 29; DB 4; Length 767;
46.3%; Pred. No. 1.3;
tive 0; Mismatches 110; Indels
                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
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STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                            38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 767 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.3
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAG1391UP
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APPLICANT: Philippsen, Peter
APPLICANT: Pohlman, Rainer
APPLICANT: Stelner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Racchie, Philipp
APPLICANT: Racchie, Philipp
APPLICANT: Rechischung, Corinne
TITLE OF INVENTION: GENONIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEPRAX: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 1.3;
0; Mismatches
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Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/808,793
                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 566, Application US/08998416 Patent No. 6239264
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No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 6519 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.9%;
Matches 46; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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US-08-808-793-24
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                                            New York
: USA
                      Rochester
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                                                                     COUNTRY:
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126 ttccgccccttcacttccgactctctggctgcaattgagaagcggattgccatccaaaag 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES; 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793
                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                              34,103
FR: 19603/601(CRFD-1657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19603/1062 (D-1906A)
                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Score 28.8; D. Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US, 60/034, 361
24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08808793
Patent No. 5858713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET UNMBER: 196
TELECOMMUNICATION:
TELEPHONE: 716-263-1636
                                                                              REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION-
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                 ch 9.6%;
1 Similarity 52.5%;
63; Conservative
                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTORNEY/AGENT INFORMATION:
                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              LENGTH: 6315 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                   Braman, Susan J.
                                                                                                                                                                 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abbit
STREET: Clinc
CITY: Rochester
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                       US-08-772-512A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 TICCGICCCTICACCCGCGAATCATTGTTACAAATCGAACAACGTATCGCTGAACATGAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6315;
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ZIF: 14603.

ZIF: 14603.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

""""ANTON NUMBER: US/08/772,512A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALESSEE: MIXON, HARGRAVE, DEVANS & DOYLE LLP
FEET P.O. Box 1051, Clinton Square
(: Rechester
E: New York
**RY: USA
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                        19603/1062 (D-1906A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.8;
Pred. No. 4
                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 24.05 60/034,361
FILING DATE: 24.0EC-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER: US 60/012,649
                                                                                                                                                                                                               FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
TORNEY ARCHITECT
                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08772512A Patent No. 6022705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Indpele, Particia J.
TITLE OF INVENTION: INSECT SODI.
TITLE OF INVENTION: INSECTICIDE-
TITLE OF INVENTION: FLIES
NUMBER OF SOUNCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    ATTOREX/AGENT INFORMATION:
NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/COCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6315 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: CDNA
US-08-808-793-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 63; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-772-512A-2
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APPLICANT: PRITCHARD, MELANIE
TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE
TITLE OF INVENTION: DOWN SYNDROM CRITICAL REGION OF HUMAN CHROMOSOME 21,
TITLE OF INVENTION: IDENTIFIED BY A NEW "ALU-SPLICING PCR" TECHNIQUE,
TITLE OF INVENTION: CODING PROLINE-RICH PROTEIN (DSCR1) HIGHLY
TITLE OF INVENTION: EXPRESSED IN FOETEL BRAIN AND IN HEART AND METHOD
TITLE OF INVENTION: FOR CHARACTERIZING IT.
                                                                                                                                                                   106 AAACAAAAGGAGCTGGAAAGAAGAAGAGCCGCCGAAGGAGGAGCAGATACGATATGATGAC 165
                                                                                                                              186 gagaaaaagaagtetaaagaecagaeaggagaagtaeceeageeteaaeeteagettgae 245
                                             126 ttccgcccttcacttccgactctctggctgcaattgagaagcggattgccatccaaaag 185
                                                                                    46 TTCCGTCCTTCACCCGCGAATCATTGTTACAAATCGAACGTATCGCTGAACATGAA 105
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain
    57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 21/YAC 72H9
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMEDIATE SOURCE: gene library of cDNA LIBRARY: gene library of cDNA from fc CLONE: BC-17.8-1 and BC-17.8-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1 FOR DOS
CURRENT APPLICATION DATA:
FILING DATE: JUNE 7, 1996
                                                                                                                                                                                                                                                                                                                                      APPLICANT: ESTIVILL PALLEJA, XAVIER APPLICANT: FUENTES, JUAN JOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ES P9501140
FILING DATE: JUNE 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: JANET I. CORD
REGISTRATION NUMBER: 33,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDNA for mRNA, BC-17.8
                                                                                                                                                                                                                                                                           Sequence 1, Application US/08665040 Patent No. 5869318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61ST STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
ORCENOPMENTAL STAGE: foetal
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP POSITION: 21q22.1-q22.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA for mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2174 base pairs
    63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N
COUNTRY:
                                                                                                                                                                                                                                                          ÚS-08-665-040-1
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                               126 ttccgcccttcacttccgactctctggctgcaattgagaagcggattgccatccaaaag 185
                                                                                                                                                                                                                                                                                                                     186 gagaaaaagaagtctaaagaccagacaggagaagtaccccagcctcaacctcagcttgac 245
                                                                                                                                                                                                                                                                                                                                                                                                                       106 AAACAAAAGGAGCTGGAAAGAAAGAAGCCGCCGAAGGAGGAGCAGATACGATATGATGAC 165
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                 Length 6318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6318;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP: P.O. Box 1051, Clinton Square Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,512A
                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19603/601(CRFD-1657)
                                                                                                                                                                                                            Score 28.8; DB Pred. No. 4.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%; Score 28.8; Dl 52.5%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,618
FILING DATE: 01-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/08772512A
; Patent No. 6022705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                            Query Match 9.6%;
Best Local Similarity 52.5%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 6318 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 6318 base pairs
                                                               nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                          ; MOLECULE TYPE: CDNA
US-08-808-793-1
                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-772-512A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-772-512A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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DSCR1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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    deduced protein
    proline-rich protein domains
    glutamic acid-rich protein domains
    leucine/phenylalanine-rich protein domains

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9.6%; Score 28.6; DB 2; Length 2174;
Best Local Similarity 59.0%; Pred. No. 3.1;
Matches 49; Conservative 0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                   NAME/KEY: coding sequence
LOCATION: 49..560
OTHER INPORMATION: Down Syndrome critical
FEACUTE:
NAME/KEY: DSCR1
LOCATION: 1..71 PEPTIDES
IDENTIFICATION METHOD: translation of the
OTHER INFORMATION: - deduced protein
OTHER INFORMATION: - proline-rich protein
OTHER INFORMATION: - glutamic acid-rich protein
OTHER INFORMATION: - glutamic acid-rich protein
OTHER INFORMATION: - leucine/phenylalanine-ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 poly (A)
1541..1546 AND 2132..2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      untranslated 5'1..48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        untranslated 3'
564..2174
     1..2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: U.
LOCATION:
FEATURE:
NAME/KEY: 2
LOCATION:
U.OCATION:
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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Search completed: February 26, 2002, 22:39:47 Job time: 17247 sec

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Gencore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 20:07:03; Search time 5057.4 Seconds (without alignments)
635.304 Million cell updates/sec

Title: US-09-646-224A-3

Berfect score: 299
Sequence: 1999
Scoring table: DENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874
Minimum DB seq length: 2000000000

Maximum Match 1004
Maximum Match 1004
Listing first 45 summaries
```

17: em_gss_ptn:* 18: em_gss_pro:* 19: em_gss_rod:* 20: em_gss_orther:* 21: em_gss_other:* 21: em_gss_other:* and is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_fun:* em_gss_hum:* em_gss_inv:*

em_estfun:*
em_esthum:*
em_esthum:*
em_estpl:*
em_estpl:*
em_estpo:*
em_estro:*
em_estro:*
em_estro:*
gb_estl:*
gb_estl:*
gb_estl:*
gb_htc:*
gb_htc:*

EST:*

Database :

| | | | | | SUMMARIES | |
|--------|-------|-------|-------------------|------|-----------|----------------------|
| | | ф | | | | |
| Result | | Query | | | | |
| SO. | Score | Match | e Match Length DB | DB | ΙD | Description |
| П | 39 | 13.0 | 491 | 11 | | . BF600973 265816 MA |
| 2 | 39 | 13.0 | | 11 | BF706700 | BF706700 281320 MA |
| m | 39 | 13.0 | | 10 | BE485569 | BE485569 172639 BA |
| 4 | 39 | 13.0 | | 10 | BE752960 | BE752960 205802 MA |
| S | 39 | 13.0 | | 10 | AW654550 | AW654550 104076 MA |
| 9 | 35.2 | 11.8 | | 10 | BE685650 | BE685650 uu56h06.x |
| c 2 | 35.2 | 11.8 | | . 13 | AQ739595 | AQ739595 HS_5381_B |
| 8 | 34.6 | 11.6 | | 11 | BG663266 | BG663266 DRAAAGA02 |
| ი
ი | 34.6 | 11.6 | | 10 | BE251756 | BE251756 601112448 |
| 10 | 34.2 | 11.4 | | 10 | AV668453 | AV668453 AV668453 |
| 7 | 34 | 11.4 | 407 | 10 | AA134408 | AA134408 zo26c11.r |
| را ر | 33 | 11.3 | | 1,3 | A2017956 | A2017956 PDCT-23-2 |

| AL594553 AL594553 BE632098 UU56406.y AQ77308,182.5435_B BB471462 BB451462 AA54829 'y169f10.r AL106969 DE0xosophil AW365899 MRO-HT007 BE816689 RC5-BR023 AU170796 AU170796 BE033445 (AA_E000) BE616699 RC5-BR023 AU170796 AU170796 BE033445 (AA_E000) BG443355 (AA_E000) BG44335 (AA_E000) BG44335 (AA_E000) BG44337 (AC_E000) BG457318 U145906.x AW228737 RPCI-23-1 AU2715 TETRAGOON BF571561 602078169 BF571561 602078169 BF571561 602078169 BF582577 de31602.x AW86539 COU-UM009 AZ683152 ZM0141G20 BG408173 de69802.x AM98737 CHAISF04.r | 2222 | EST 25-APR-2001 mRNA sequence. a; Vertebrata; Euteleostomi; Ruminantia; Pecora; Bovoidea; A., Roberts, A.J., Stone, R.T., A., Fahrenkrug, S.C., Bennett A., Fahrenkrug, S.C., Bennett A., Guackenbush, J. and Ssue normalized bovine cDNA index for cattle and alt trimmed with phred and alt trimmed with phred oss_match with the -minscore 18 |
|--|--|--|
| 10 AL594553
10 BE632098
11 BA727308
11 BA727308
11 BA727308
11 BA7274308
11 CNS016NJ
11 CNS016NJ
11 AN365809
11 AN365809
11 BE816689
11 BE816689
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11 BE81689
11 BC43345
11 BC44335
11 BC44335
11 BC44335
11 BC44335
11 BC445436
11 AN214225
11 BC44636
11 AN214225
11 BF571561
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11 BC408173
11 BC408173 | 8 10
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10 | pp mRNA DS taurus cDNA 5', mR B8194 Chordata; Craniata; Cetartiodactyla; Ru B08. Se,W.M., Freking,B.A. Milte,J., Gho,J. Milte,J., Gho,J. Karamycheva,S., Lia n of four pooled-tiss ruction of a gene in 626-630 (2001) Animal Research Cent enter, NE 68933-0166, marc.usda.gov marc.usda.gov marc.usda.gov marc.usda.gov cidentified by cross, ptions. |
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1 (bases 1 to 493)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Reele, J.W.
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                                                                                                                                          /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

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Pred. No. 1;
0; Mismatches 65; Indels
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281320 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF706700
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 48390
Fax: 402 762 4390
                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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BACKWARD: GTTTTCCCAGTCACGACG
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Seq primer: ATTTAGGGGACACTATAG.
Seq primer: ATTTAGGTGACACTATAG.
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/do_xref="taxon.9913"
/do_xref="taxon.9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH109"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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1 (bases 1 to 504)
Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
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172639 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
BE485569
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Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
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Pred. No. 1;
/clone_lib="MARC 3BOV"
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Seq primer: ATTTAGGTGACACTATAG.
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Best Local Similarity 54.5%;
Matches 78; Conservative
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Query Match 13.0%;
Best Local Similarity 54.5%;
Matches 78; Conservative
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Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett, G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                 61 GGGAGATGGAGCACAGCAGTTTCTCTTTGCTGATACTGGCTGCCCTTCTCTCCCCAAG 120
                                                                                                                                                                gacagatgetacccagtaatetttecagatgageggaattteegeeeetteaetteegae 146
                                                       Gaps
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                                                                                         27 gcctcctgaggcctttctgaggatctgtggcttgtctctgtcctgagggtgaagatggat 86
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                  Length 504;
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1;
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205802 MARC 2BOV Bos taurus cDNA 5', mRNA sequence
BE752960
                                                       Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                      65;
                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1
Pred. No. 1;
0; Mismatches
                                                      0; Mismatches
                  Score 39; Di
Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGACG
Plate: 46 row: E column: 22
Seq primer: ATTTAGGGTGACACTATAG.
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                                                                                                                                                                                                                                 147 tctctggctgcaattgagaagcg 169
                                                                                                                                                                                                                                                       BE752960.1 GI:10166952
                  13.0%;
ilarity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.0%;
Best Local Similarity 54.5%;
Matches 78; Conservative
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Query Match
Best Local Similarity
Lac 78; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21180013
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ORIGIN
                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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COMMENT
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LOCUS
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KEYWORDS
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertca, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled-tissue from lymph node, ovary,
tat, hypothalamus, and pituitary."
                                                                                                             gacagatgctacccagtaatctttccagatgagcggaatttccgcccttcacttccgac 146
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                                                                                                                                                               62 GGGAGATGGAGCACAGGTTTCTCTTTGCCTGATACTGGCTGCCTTCTCTCCCAAG 121
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86
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                                gcctcctgaggcctttctgaggatctgtggcttgtctctgtcctgagggtgaagatggat
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104076 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW654550
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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0; Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
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Seg primer: ATTTAGGTGACACTATAG.
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Plate: 87 row: K column: 5
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                                                                                                                                                                                                                                                                               122 TGAATCCCCGCATTCTAAAAGTG 144
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Gaps

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Homo sapiens
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                                                                                                                                human.
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                            AQ739595/C
LOCUS
DEFINITION
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                                                                                     ACCESSION
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                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I tbases 1 to 366)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
62 GGGAGATGGAGCACGAGCAGCTTCTCTCTCTGATACTGGCTGCCCTTCTCTCCCCAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcctgagggtgaagatggatgacagatgctacccagtaatctttccagatgagcggaatt 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 tecgecectteacttecgaetectggetgeaattgagaageggattgeeatecaaaagg 186
                                                                                                                                        BE685650 366 bp mRNA EST 11-SEP-2000 uu56h06.x1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3375995 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 TCCGGAGGCGGAGGAGGATCAAGAGTTCAAAGTCATCTTCAGCTACAAATGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 GGAGACCAATCCAGACCCTCTCTCAGAAAAAGGAAAAAGGAGAAAGCAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3375995"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
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Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AGGGGAGACCGATAAAGAGAAGAAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 348.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="4 weeks"
/lab_host="DH10B"
                                         147 tctctggctgcaattgagaagcg 169
                                                                    122 TGAATCCCCGCATTCTAAAAGTG 144
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                                                                                                                                                                                                BE685650.1 GI:10073326
                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Other_ESTs: uu56h06.y1
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ilarity 52.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
                                                                                                                                                                                                                EST
                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
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                                                                                                              RESULT
BE685650
                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                VERSION
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-388
Email: yella-2887
Email: yella-2887
Email: yella-2887
Email: yellace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 957 row: P column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 9 others
                                                                                                                                                                                                                                                                                                                              Holzman,T.,
Adams,M.D. and
                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
      A GSS 16-JUL-1999
Human Male BAC Library Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 gagggtgaagatggatgacagatgctacccagtaatctttccagatgagcggaatttccg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 cccettcacttccgactctctggctgcaattgagaagcggattgccatccaaaaggagaa 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       638 GAGGTTGAGGCAGGAGAATCCTTTGAACCCAGGAGGAGGTTGCAGTGACCCGAGATAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 aaagaagtctaaagaccagacaggagagagagtaccccagctcaacctcagcttgac 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518 AAAAAAAAAAAAAAAANNAAAGNNNGGTTATACACCACGACCAAGTGCAATTTAAC
                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases I to 885)
Mahairas, G.C., Mallace, J.C., Smith, K., Swartzell, S.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Plate=957 Col=2 Row=p" /clone_lib="RPCI-11 Human Male BAC Library"
AQ739595 885 bp DNA GSS
HS_5381_B2_H01_T7A RPCI-11 Human Male BAC Library
genomic clone Plate=957 Col=2 Row=P, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.2; DB 13;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 885.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606
                                                                                AQ739595
AQ739595.1 GI:5517117
GSS.
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48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 48.6
nes 85; Conservative
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BG663266

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Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzilnae; Oryzias.
I (bases I to 518)
Naruse, K., Tanaka, M., Shima, A. and Mitani, H.
Medaka EST Project in University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: eye: vector: porB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dr priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Rit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                        Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV668453 515 bp mRNA EST 22-SEP-2000 AV668453 Sugano Kawakami 5' enriched cDNA library (OLa) Oryzias latipes cDNA clone OLa03.01f similar to intermediate filament protein ON3 (goldfish), mRNA sequence.
                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G. E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM153 row: o column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eggaattteegeeeetteaetteegaetetetggetgeaattgagaageggattgeeate 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 caaaaggagaaaaagaagtctaaagaccagacagagagaagtaccccagcctcaacctcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 CAGCAGGGTGACCAGCATGGCACTGGCCGGGCAGGAGGTGGATCTGCGTCACAGCGTTGT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-2000
                                                                                                                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                      1 (bases 1 to 581)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:355315"
/clone_lib="NH_MCC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 cttgacctaaaggcctccaggaagttgcccaactctatggc 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 TCTCCTGGTGCAGCCACCATGAACATCCACACACACTGGGGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.6; D
Pred. No. 18;
0; Mismatches
                                                                                                                                                                      Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 578 Location/Qualifiers
                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, F
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV668453.1 GI:9933198
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50.9%;
                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.6
Best Local Similarity 50.9
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       1. .581
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                        Homo sapiens
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    human.
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                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EASE COUNT
ORIGIN
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AUTHORS
TITLE
                      ORGANISM
                                                                                                      AUTHORS TITLE JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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AV668453
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                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                       PATURES
  SOURCE
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                                                                                                                                                                                                                                                         Xiao, H.S., Han, Z.G., Zhang, F.X., Huang, Q.H., Lu, Y.J., Bao, L., Fu, G., Guo, C., Yan, Q., Jin, S.X., Zhu, Z.D., Xu, X.R., Li, N.G., Chen, Z. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang4lon.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                           Euteleostomi;
  400 bp mRNA EST 30-APR-2001
Rat DRG Library Rattus norvegicus CDNA clone DRAAAGA02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE251756 581 bp mRNA EST 13-JUL-2000 601112448F1 NIH_MGC_16 Homo sapiens CDNA clone IMAGE:3353315 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 attgagaagcggattgccatccaaaaggagaaaaagaagtctaaagaccagacaggagaa 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ACTAATCAGTGTTTTGACATCGAAGAGGAGGTGTCCAAGTATCAAGACTACACTAACGAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                  Distinct gene expression profiles of rat dorsal root ganglion induced by peripheral nerve axotomy Unpublished (2001)
30-APR-2001
                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleost
Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 gtaccccagcctcaacctcagcttgacctaaaggcctccaggaagttgcccaactctatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="dorsal root ganglion"
/dev_stage="adult"
85 c 96 g 85 t l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Rat DRG Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"DRAAAGA02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: xu.zhang@ion.ac.cn
                                                                                  BG663266.1 GI:13885188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BE251756
BE251756.1 GI:9121887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%;
54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                       (bases 1 to 400)
                                            5', mRNA sequence.
BG663266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.6
Best Local Similarity 54.3
Matches 70; Conservative
                                                                                                                              Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                    DRAAAGA02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                   Rattus.
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                                                                                                          EST
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AZ017956/c
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1 (bases 1 to 407)

Hiller, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hullman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Milson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                    enriched cDNA library (OLa
              Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4440
Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Sugano-Rawakami 5' end enriched cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GGTTCCTTCAATCCAACGATCACAGCCGTCCATGTCAACCAGAGCCTGCTGGCCCCTCTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 agggtgaagatgatgacagatgctacccagtaatctttccagatgagcggaatttccgc 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 ccettcacttccgactctctggctgcaattgagaagcggattgccatccaaaaggagaaa 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 TCCCTCAACAACGGCTTTGCGACTTTCATCGACAAGGTCCGTTTCCTGGAGCAGCAGAAC 430
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IMAGE:588020 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 515;
                                                                                                                                                                                                                                                                                                                                                            others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 103;
                                                                                                                                                                                                                                                                                    2,
                                                                                                                                                                                                                                                                                    /clone_lib="Sugano Kawakami
                                                                                                                                                                                                          /organism="Oryzias latipes"
/strain="HNI"
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                                                                                                                                                                                                                                                                                                                                                          115
                                                                                                                                                                                                                                                                                                                   /tissue_type="whole body"
/dev_stage="adult"
152 c 108 g 115
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34.2;
Pred. No. 24
                                                                                                                                                                                                                                             /db_xref="taxon:8090"
/clone="0La03.01f"
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48.2%;
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 Unpublished (2000)
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AZU17956 504 bp DNA GSS 25-FEB-2000
RPCI-23-259K13.TV RPCI-23 Mus musculus genomic clone RPCI-23-259K13
AZ017956
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other. GSSS: RPCI-23-259K13.TJ
Contact: Shaying Lao
Contact: Shaying Lao
Contact: Shaying Research
9712 Medical Center Dr., Rockville, MD 20850, USA
The: 301 838 0200
Fex: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhaofeigr.org
Clones are derived from the mouse BAC library RPCI:23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/Dac_ends/mouse/bac_end_intro.html
Plate: 259 row: K column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 504)
                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor" //tissue_type="tumor" //tissue_type="tumor" //cell_line="TB4 carcinoma cell line" //lab_host="Solk cells (Knamycin resistant)" //lab_host="Solk cells (Knamycin resistant)" //note="forgan : colon: Vector: pBluescript SK-; Site_l: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. T-84 colonic epithelial cell line. Average insert size: 1.0 kb; Uni_ZAP XR Vector; -5' adaptor sequence: 5' CAATTCGCCACGAG 3' -3' adaptor sequence: 5'
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 840 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 others
                                                                                                                                                                                                                      /db_xref="CDB:4620322"
/db_xref="taxon:9606"
/clone="IMAGE:588020"
/clone_lib="Stratagene colon (#937204)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 10;
Pred. No. 27;
0; Mismatches 32
                                                                                  Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 385.
Location/Qualifiers
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                                                                                                                                                                                                       sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 gagggtgaagatggatgacagatg 94
                                                                                                                                                                                                 /organism="Homo
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Best Local Similarity 61.9%;
Matches 52; Conservative
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                                                                                                                                                                             1. .407
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Class: BAC ends
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Gaps

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3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 386, NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pcs107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1085599
                                                                                                                                                                                                                                         126 ttccgcccttcacttccgactctctggctgcaattgagaagcggattgccatccaaaag 185
                                                                                                                                                                                                                                                               BE632098 386 bp mRNA EST 25-AUG-2000 uu56h06.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3375995 5', mRNA sequence.
                                                                                                                                                               Length 684;
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                                                                                                                                                             DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_thymus_2NbMT"
/sex="male"
                                                                                                                                                           Score 33.8; DE Pred. No. 31; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred., No. 34;
0; Mismatches
                                                                                 182
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3375995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                               149 g
                                                                                                                                                                                                                                                                                                                    186 gagaaaaagaagtctaaagaccaga 210
                                                                                                                                                                                                                                                                                                                                                         248 AATAAAAGCCACCAAGAGAAGACA 272
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51.3%;
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ilarity 62.4%;
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Best Local Similarity 51.3
Matches 78; Conservative
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                                                                 end.
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hes 53; Conserv
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Best Local
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                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CooR; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially diagested
with a combination of EcoRI and EcoRI methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BHOB electrocompetent cells (BRL Life Technologies).
92 c 100 g 161 t
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AL594553 XGC-gastrula Silurana tropicalis cDNA clone TGas001a17 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="rcas001a17"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="scherichia coli DH10B"
/note="Vector: pC5107; Site_l: EcoRI; Site_2: NotI; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xehopodinae; Silurana.
1 (bases 1 to 684)
Huckle, E., Taylor, R., McMurray, A., Ashurst, J.L., Zorn, A.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgtctctgtcctgagggtgaagatggatgacagatgctacccagtaatctttccagatga 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 TGTGTGTGTTCTGGGGATCAAACTAGAGGCCTCAATGGAGGGCATATACTCTACAAATGA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 gcggaatttccgcccttcacttccgactcttggctgcaattgagaagcggattgccat 178
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TROPICALIS_SEQUENCE_ID: TGas001a17.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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0
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Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Silurana tropicalis"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Score 33.8; 1
Pred. No. 31;
                                                                                                /clone="RPCI-23-259K13"
/clone_lib="RPCI-23"
                                      /organism="Mus musculus
                                                                             /db_xref="taxon:10090"
    Location/Qualifiers
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                                                                                                                                                           /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL594553.1 GI:15006614
                                                                                                                                         /sex="Female"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 591) Mahalaras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBACe3.6; Site_1: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"

149 c 125 g 193 t 19 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1011 row: 1.
                                                                                                                                                                                                                                                                                                                                                               AQ727308 591 bp DNA GSS 14-JUL-1999 HS_5435_B1_F06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1011 Col=11 Row=L, DNA sequence.
67 tcctgagggtgaagatggatgacagatgctacccagtaatctttccagatgagcggaatt 126
                              127 tecgeceetteaettecgaetetetggetgeaattgagaageggattgeeateeaaaagg 186
                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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/clone="Plate=1011 Col=11 Row=L"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
761: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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                                                                                                                                                                                         187 agaaaaagaagtctaaagaccagacaggagaa 218
                                                                                                                                                                                                                                         137 AGGGGGAGACCGAGAAGAGAGGGGAAGGA 106
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Seq primer: T7
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ilarity 52.2%;
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236 tcagcttgacctaa 249

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